

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: August 8, 2001, 00:14:24 ; Search time 52.75 Seconds  
(Without alignments)  
514.873 Million cell updates/sec

Title: US-09-670-568B-1

Perfect score: 2383  
Sequence: 1 MSQSTQTEFLSPSEVFQHIW.....PKSDVFRHSPKPRSYYP 448

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A.Geneseq\_0601:\*  
1: /cgnl\_9/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
2: /cgnl\_9/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
3: /cgnl\_9/gcgdata/geneseq/geneseq/AA1982.DAT:\*  
4: /cgnl\_9/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
5: /cgnl\_9/gcgdata/geneseq/geneseq/AA1984.DAT:\*  
6: /cgnl\_9/gcgdata/geneseq/geneseq/AA1985.DAT:\*  
7: /cgnl\_9/gcgdata/geneseq/geneseq/AA1986.DAT:\*  
8: /cgnl\_9/gcgdata/geneseq/geneseq/AA1987.DAT:\*  
9: /cgnl\_9/gcgdata/geneseq/geneseq/AA1988.DAT:\*  
10: /cgnl\_9/gcgdata/geneseq/geneseq/AA1989.DAT:\*  
11: /cgnl\_9/gcgdata/geneseq/geneseq/AA1990.DAT:\*  
12: /cgnl\_9/gcgdata/geneseq/geneseq/AA1991.DAT:\*  
13: /cgnl\_9/gcgdata/geneseq/geneseq/AA1992.DAT:\*  
14: /cgnl\_9/gcgdata/geneseq/geneseq/AA1993.DAT:\*  
15: /cgnl\_9/gcgdata/geneseq/geneseq/AA1994.DAT:\*  
16: /cgnl\_9/gcgdata/geneseq/geneseq/AA1995.DAT:\*  
17: /cgnl\_9/gcgdata/geneseq/geneseq/AA1996.DAT:\*  
18: /cgnl\_9/gcgdata/geneseq/geneseq/AA1997.DAT:\*  
19: /cgnl\_9/gcgdata/geneseq/geneseq/AA1998.DAT:\*  
20: /cgnl\_9/gcgdata/geneseq/geneseq/AA1999.DAT:\*  
21: /cgnl\_9/gcgdata/geneseq/geneseq/AA2000.DAT:\*  
22: /cgnl\_9/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2383	100.0	448	20	AAV45246
2	2383	100.0	448	20	AAV05958
3	2383	100.0	448	21	AAAB11359
4	2296	96.3	483	20	AAV05961
5	2185	91.7	516	20	AAV05954
6	2185	91.7	516	21	AAAB11363
7	2185	91.7	641	20	AAV45247
8	2185	91.7	641	20	AAV05953
9	2185	91.7	641	21	AAAB11358
10	2185	91.7	680	21	AAAB11361
11	2185	91.7	680	21	AAV50997

12	2169	91.0	680	20	AAV05958	Human cell regulat
13	2169	91.0	680	21	AAV50998	Rat KET protein.
14	2011	84.4	393	20	AAV05957	Human cell regulat
15	1938	81.3	389	20	AAV05964	Human cell regulat
16	1813	76.1	461	21	AAAB11362	Human p53 regulat
17	1813	76.1	586	20	AAV05956	Human cell regulat
18	1811	76.0	461	20	AAV05963	Mouse cell regulat
19	1811	76.0	586	20	AAV05962	Mouse cell regulat
20	1796	75.4	356	20	AAV43135	Human p40 protein
21	1796	75.4	356	21	AAAB11360	Human p53 protein
22	1796	75.4	586	21	AAAB11357	Human p63 protein
23	1789	75.1	586	20	AAV41032	Human lung tumor a
24	1789	75.1	586	21	AAAB11317	Human lung cancer-
25	1297.5	54.4	499	21	AAV44635	Human p53 tumor s
26	1297.5	54.4	499	21	AAV44635	Human p53 beta spl
27	1287.5	54.4	635	20	AAV30661	Human NBS-1 alpha
28	1287.5	54.4	636	18	AAV36184	Human p53 tumor s
29	1297.5	54.4	636	21	AAV44634	Human p73 alpha sp
30	1296.5	54.4	499	18	AAV36183	Monkey p53 tumor
31	1296.5	54.4	636	21	AAV50999	Human p73 protein.
32	1286.5	54.4	637	18	AAV36182	Monkey p53 tumor
33	1279.5	53.7	589	18	AAV36185	Mouse p53 tumor s
34	1251	52.5	506	18	AAV36188	Human p53 tumor s
35	1248.5	52.4	587	18	AAV36187	Human p53 tumor s
36	1248.5	52.4	588	18	AAV36189	Human p53 tumor s
37	722.5	30.3	393	20	AAV57244	Human p53 protein.
38	722.5	30.3	393	20	AAV84270	Human p53 protein.
39	717.5	30.1	355	18	AAV13950	Del356-393 modifie
40	717.5	30.1	363	18	AAV13950	Modified p53 varia
41	717.5	30.1	393	13	AAV22238	Sequence of 53 kd
42	717.5	30.1	393	13	AAV22238	p53. Synthetic.
43	717.5	30.1	393	16	AAV46223	p53 protein. Homo
44	717.5	30.1	393	16	AAV79658	Human p53 protein.
45	717.5	30.1	393	19	AAV48658	Amino acid sequenc

## ALIGNMENTS

RESULT 1	AAV45246	standard; Protein: 448 AA.
ID	AAV45246	
XX	AAV45246;	
AC	07-JAN-2000	(first entry)
XX		
DE	Human p51 protein A.	
XX		
KW	Human: p51; p53 related gene; cell proliferation; regulation; cancer;	
KW	tumor suppression; diagnosis.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Domain	1..59
FT	Domain	/label= transactivation_domain
FT	Domain	142..321
FT	Domain	/label= DNA_binding_domain
FT	Domain	353..397
FT	Domain	/label= oligomerisation_domain
XX		
PN	W09950412-A1.	
XX		
PD	07-OCT-1999.	
XX		
XX	24-MAR-1999;	99MO-JP01512.
XX		
PR	27-MAR-1998;	98JP-0100467.
XX		
PA	(SAKA ) OTSUKA PHARM CO LTD.	
PA	(IKAW/) IKAWA Y.	
XX		

PI Ikawa Y, Ikawa S, Oinata M;  
XX WPI: 1999-591318/50.  
DR N-PSDB: AAZ25770.  
XX

PT New p53 related human gene p51, useful for diagnosis, investigation and  
PT treatment of cancers and screening for potential cell proliferation  
agents -

XX Claim 1: Page 147-148; 163pp: Japanese.

XX The present sequence represents a human p51 protein, which is related to  
CC p53 and has cell proliferation regulation and tumour suppression  
CC activity. The p51 gene can be used in the investigation, diagnosis and  
CC treatment of diseases such as cancer, with which the p53 family cell  
CC proliferation regulation is associated. The p51 protein may be used for  
CC screening potential agonists and antagonists of its regulatory function,  
CC for use as drugs,  
XX

SO Sequence 448 AA:

Query Match 100.0%; Score 2383; DB 20; Length 448;  
Best Local Similarity 100.0%; Pred. No. 2,1e-207;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSGSTQTNFEFLSPVQOHIMWDLFQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60
DB 1 msqstqtnfeiflspvqohimwdlfepicvqpidlnfvdesedgatnkiesmdcirmq 60
QY 61 DSDLSDPMPQYTNGLNSMDQIQNGSSSPYNTDHAONSVAAPSPYQPSSTPDAL 120
DB 61 ddsldspmpqytnlglnsmdqiqngssspyntdhaonsvappspystpdal 120
QY 121 SPSPALPSTWDYPCGPHSDVSPFOQSTAKSATWTYSTEKLKLYCOIAKTCPIQIVWMP 180
DB 121 spspalpstwdypcghsdvspfoqstaksatwtysteklkycoiaktcpiqivwmp 180
QY 181 PGAVIRAMPYVKKAEHTEVVKRCRNHFLSRFNEGQIAPPSHLIRVEGNSHAQYEDP 240
DB 181 pgavirampyvkkaehtevvrkrcrnfhlsrfnegqiappshlirvegnsahayedp 240
QY 241 ITGROSVLWVPEPPVQTEFTTLYLNFMCNSCVGGMNRPLIIVLTETEDGOVIGRRC 300
DB 241 itgrsvlwvpeppvqtefttlylnfmcnscvvgmmnrplilvltetdgvigrrc 300
QY 301 FPARICACGPRKADSDSIRKQVSDSTKNGDGTKRPFQNTGCIQMTSIRKRRSPDE 360
DB 301 fparicacgprkadedsirkoysdstkngdgtkrpfqntgciqmtsirkrspde 360
QY 361 LLYLPVGRRETYEMDLKTESLELMQYLPQRTIEFYRQOOQOHOHLQKLLSACFRNE 420
DB 361 llylpvgrretyemdlkteslelmqylpqrtefyroooqoohohlqkllsacfrne 420
QY 421 LVEPRERTRKQSDVFRFKSKPPNRSVYP 448
DB 421 lvepretrkqsdvfrfkspknrsyvp 448

```

RESULT 2  
AA05955  
ID AA05955 standard; Protein: 448 AA.

XX AA05955;  
XX

XX 16-AUG-1999 (first entry)  
XX

XX Human cell regulatory protein p63, isoform hUTAP63 gamma.  
XX Cell regulatory protein; p63; hUTAP63 gamma; Tap63 gamma; human;  
KW cancer; tumour suppressor; cell cycle control; apoptosis;  
KW cell proliferation; cell differentiation; therapy.  
XX

OS Homo sapiens.

XX W09919357-A2.

XX 22-APR-1999.

XX 02-OCT-1998; 98WO-US21992.

XX 29-MAY-1998; 98US-0087216-  
PR 15-OCT-1997; 97US-0062076.

XX (HARD) HARVARD COLLEGE

XX Mckeeon F, Yang A;

XX WPI: 1999-277595/23.  
DR N-PSDB: AAX58574.

XX New isolated p63 cell regulatory protein for, e.g. treatment of  
PT tumours

XX Claim 23: Fig 11: 161pp; English.

XX The present invention concerns the discovery of a new family of  
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,  
CC which demonstrate certain sequence identity to known tumour  
CC suppressor proteins p53 and p73. It has been observed that the  
CC intron-exon organisation is conserved between p73 and p53, and from  
CC known exon and intron sizes for these 2 genes, it was possible to  
CC identify new members of this gene family using a PCR-based strategy  
CC of amplifying 2 exons in a conserved domain and their intervening  
CC intron. The human p53 gene was localised to chromosomal position  
CC 3q27-29. At least 6 different isoforms exist. Splice variants  
CC differing at the C-terminus have been designated as alpha, beta and  
CC gamma forms, while p63 members have been designated as delta and  
CC designated as delta and gamma forms, where the delta form lacks the  
CC transactivation domain. The present sequence represents human  
CC p63 isoform Tap63 gamma. p63 was detected in a variety of  
CC human and mouse tissue. It demonstrates remarkably divergent  
CC activities, such as the ability to transactivate p53 reporter genes  
CC and induce apoptosis. Cessation or down-regulation of p63 expression  
CC may play a critical role in the process of cervical squamous  
CC differentiation, both benign and neoplastic. Delta isoforms of p63  
CC act as dominant negatives towards transactivation by p53 and p63.  
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.  
CC cachexia) and neuronal differentiation and related degenerative  
CC disorders. p63 polypeptides (see AA05953-64), polynucleotides (see  
CC AA58572-83) and anti-p63 antibodies of the invention can be used to  
CC identify compounds useful for treating disorders involving such  
CC processes, in detection and diagnosis, and in the production of  
CC transgenic animals.  
XX

SO Sequence 448 AA:

Query Match 100.0%; Score 2383; DB 20; Length 448;  
Best Local Similarity 100.0%; Pred. No. 2,1e-207;  
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSGSTQTNFEFLSPVQOHIMWDLFQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60
DB 1 msqstqtnfeiflspvqohimwdlfepicvqpidlnfvdesedgatnkiesmdcirmq 60
QY 61 DSDLSDPMPQYTNGLNSMDQIQNGSSSPYNTDHAONSVAAPSPYQPSSTPDAL 120
DB 61 ddsldspmpqytnlglnsmdqiqngssspyntdhaonsvappspystpdal 120
QY 121 SPSPALPSTWDYPCGPHSDVSPFOQSTAKSATWTYSTEKLKLYCOIAKTCPIQIVWMP 180
DB 121 spspalpstwdypcghsdvspfoqstaksatwtysteklkycoiaktcpiqivwmp 180
QY 181 PGAVIRAMPYVKKAEHTEVVKRCRNHFLSRFNEGQIAPPSHLIRVEGNSHAQYEDP 240
DB 181 pgavirampyvkkaehtevvrkrcrnfhlsrfnegqiappshlirvegnsahayedp 240

```

Db 181 pggavirampyvkkaehvtevkrcpnhejsrefnegqlappshllirvegnshaqyvedp 240  
 QY 241 ITGKQSVLVPEPPQVGTETFTVLVNFMCNNSCVGGMNRRPILITVLTETDGOVLGRRC 300  
 Db 241 itgqsvlvpeppqvgtetftvlnfmcnscvvgmmrrpiliivltetdgvlgrrc 300  
 QY 301 FEARICACPGRRKRADEDSIRKQOVSDSTKNGDGTKRPFRRONTGCIOWTSIKRRSPDE 360  
 Db 301 fearicacpgrrkadedsirkqovsdstkngdgtkrpfrrnhtgicmstikrrspde 360  
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIFTYRQOQOQHLLQKHLLSACFRNE 420  
 Db 361 llylpvgrretyemllkikeslelmqylpqhtlelyrqgqgqbhlqkhlisacfrne 420  
 QY 421 LVEPRRETPKQSDVFFRRSKPPNRSVYP 448  
 Db 421 lveprretpkgsdvffrrskppnrsvyp 448

## RESULT 3

AAB1359

ID AAB1359 standard; Protein; 448 AA.

AC AAB1359;

DT 21-FEB-2001 (first entry)

DE Human p63 protein isoform #3.

KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;

KM vaccine; detection.

OS Homo sapiens.

PN W0200061612-A2.

PD 19-OCT-2000.

PF 03-APR-2000; 2000MO-US089896.

PR 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

PA (CORI-) CORIXA CORP.

PI Wang T, Fan L;

XX WPI: 2000-628399/60.

DR N-PSDB; AAC66029.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 100.0%; Score 2383; DB 21; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 2, 1e-207;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQINELISPEVFOHIMWLEDPICSVOPIDLNVEDESEDAIKIEISMDICRMQ 60  
 Db 1 msqstqinefispvfgqhwllfegplicesvqpldnfvedesdgatnkliemdcirmq 60  
 QY 61 DSDLSDPKMPQYTNLGLNSMDQOIONGSSSTSPYNDHQNSTVTAQSPVAPSPSTPAL 120  
 Db 61 dsdlsdpmpqytnlglinsmdqoiongssstspyncthaqnsylvapsyqpsstpal 120  
 QY 121 SPSPAIPESTNDYGPSPHSDVSEFOOSSTFAKSAWTYSTELKLYCOIAKTCPIQIKVMTTP 180  
 Db 121 spspaipestdypghsfdsfsgstakstwtysteikllycoiaktcpiqikvmttp 180  
 QY 181 PGAVIRAMPYVKKAHEHTEVVKRCPNHELSREFNEGOIAPSHLIRVEGNSHAQYVEDP 240  
 Db 181 pggavirampyvkkaehvtevkrcpnhejsrefnegqlappshllirvegnshaqyvedp 240  
 QY 241 ITGKQSVLVPEPPQVGTETFTVLVNFMCNNSCVGGMNRRPILITVLTETDGOVLGRRC 300  
 Db 241 itgqsvlvpeppqvgtetftvlnfmcnscvvgmmrrpiliivltetdgvlgrrc 300  
 QY 301 FEARICACPGRRKRADEDSIRKQOVSDSTKNGDGTKRPFRRONTGCIOWTSIKRRSPDE 360  
 Db 301 fearicacpgrrkadedsirkqovsdstkngdgtkrpfrrnhtgicmstikrrspde 360  
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIFTYRQOQOQHLLQKHLLSACFRNE 420  
 Db 361 llylpvgrretyemllkikeslelmqylpqhtlelyrqgqgqbhlqkhlisacfrne 420  
 QY 421 LVEPRRETPKQSDVFFRRSKPPNRSVYP 448  
 Db 421 lveprretpkgsdvffrrskppnrsvyp 448

## RESULT 4

AAV05961

ID AAV05961 standard; Protein; 483 AA.

AC AAV05961;

DT 16-AUG-1999 (first entry)

DE Mouse cell regulatory protein p63, isoform mutAp63 gamma.

KW Cell regulatory protein; p63; mutAp63 gamma; TAp63 gamma; mouse;

KM cancer; tumour suppressor; cell cycle control; apoptosis;

XX cell proliferation; cell differentiation; therapy.

OS Mus sp.

PN W09919357-A2.

PD 22-APR-1999.

PF 02-OCT-1998; 98MO-US21992.

PR 29-MAY-1998; 98US-0087216.

PR 15-OCT-1997; 97US-0062076.

PA (HARD ) HARVARD COLLEGE.

PI McKeon F, Yang A;

XX WPI: 1999-277595/23.

DR N-PSDB; AAX58580.

XX

XX

New isolated p63 cell regulatory protein for, e.g. treatment of tumours

PS Claim 23; Fig 17; 161pp; English.

CC The present invention concerns the discovery of a new family of  
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,  
CC which demonstrate certain sequence identity to known tumour  
CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using  
CC RACE. Sequencing of the amplification product indicated that the  
CC amplified cDNA possessed a truncated N-terminus, i.e. the  
CC transactivation domain was absent. Additional splice variants were  
CC identified by screening a cDNA library with a probe corresponding  
CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice  
CC variants differing at the C-terminus are designated as alpha, beta  
CC and gamma forms, while p63 members differing in the N-terminus are  
CC designated as delta and TA forms, where the delta form lacks the  
CC transactivation domain. The present sequence represents murine  
CC p53 isotype mutap63 gamma. p63 was detected in a variety of  
CC human and mouse tissue. It demonstrates remarkably divergent  
CC activities, such as the ability to transactivate p53 reporter genes  
CC and induce apoptosis. Cessation or down-regulation of p63 expression  
CC may play a critical role in the process of cervical squamous  
CC differentiation, both benign and neoplastic. Delta isoforms of p63  
CC act as dominant negatives towards transactivation by p53 and p63.  
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.  
CC cachexia) and neuronal differentiation and related degenerative  
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see  
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to  
CC identify compounds useful for treating disorders involving such  
CC processes, in detection and diagnosis, and in the production of  
CC transgenic animals.

CC Sequence 483 AA;

Query Match 96.3%; Score 2296; DB 20; Length 483;

Best Local Similarity 96.9%; Pred. No. 1.8e-199;

Matches 434; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDINFVDESEDAATNKIEISMDCIIMQ 60  
DB 40 msqstqetneflspsvfgqhlwdfleqplcsvqpldlnfvdpsengatnkietmdclmq 99  
QY 61 DSDLDPMKPYQTNTGLNSMDQIQNGSSSTSPYNTTHAQNSTVAPSPYAPSPSTFAL 120  
DB 100 dsdlldpmkpyqtnlgnlsmdqiqngssstspynthaqnsvapspypspstfai 159  
QY 121 SSPPAIPSTNDPGRHSFVSPQOSTAKSATWTSTELKRLKCOIATKCPQIOIKVTMP 180  
DB 160 spspaiptndtppghsfvdfvsgstakstwtstlklkycqiaktcpqlkvmtpp 219  
QY 181 PGGAIVIRAMPYKKAHTEVVKRCPNHELSEFNEGOTAPPSHLIRVEGNSHAQYVEDP 240  
DB 220 pggavirampyvkkaehylevkrpcpnhelisrefnegqlapshlirvegnshaqyvedp 279  
QY 241 ITGRGOSVIVPYPPOVGRFTVTLYNPMCNSSCVGNMRPRLITVLTETRGQVIGRC 300  
DB 280 itgrgsivivpypvpgvgrftvtlynmcnsscvgnmrprllitvltctrgqvligrc 339  
QY 301 FEARICACGPRKADKDESIKQOVSSTKNGDGTGRPFQNTHTGIOMTSIKKRSPPDE 360  
DB 340 fearicacgprkadedstirkqovsdtknkgdgtgrpfqnthtgiomtsikkrsppde 395  
QY 361 LLYLTVKRGRTYEMILKTESLMOYLPORTIETRYRQOQOQOHLLQKHLISCFRNE 420  
DB 396 llyltyvkrgrtyemilktesiymoylportietryrqoqoqhllqkhlisacfne 455  
QY 421 IVEPRREPQKSDVFFRHSKPPNRSVYP 448  
DB 456 iveprrepqksgdvffrhnppnhsvyp 483

RESULT 5  
AAY05954  
ID AAY05954 standard; Protein; 516 AA.

XX AAY05954;

AC 16-AUG-1999 (first entry)

DT Human cell regulatory protein p63, isoform huTap63 beta.

DE Cell regulatory protein; p63; huTap63 beta; Tap63 beta; human;

KW cancer; tumour suppressor; cell cycle control; apoptosis;

KW cell proliferation; cell differentiation; therapy.

OS Homo sapiens.

XX MO9919357-A2.

XX 22-APR-1999.

XX 02-OCT-1998; 98MO-US21992.

XX 29-MAY-1998; 98US-0087216.

XX 15-OCT-1997; 97US-0062076.

XX (HARD ) HARVARD COLLEGE.

XX MCKEON F, Yang A;

XX WPI: 1999-277595/23.

XX N-PsDB; AAX58573.

XX New isolated p63 cell regulatory protein for, e.g. treatment of

XX tumours

XX Claim 23; Fig 10; 161pp; English.

CC The present invention concerns the discovery of a new family of  
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,  
CC which demonstrate certain sequence identity to known tumour  
CC suppressor proteins p53 and p73. It has been observed that the  
CC intron-exon organisation is conserved between p73 and p53, and from  
CC known exon and intron sizes for these 2 genes, it was possible to  
CC identify new members of this gene family using a PCR-based strategy  
CC of amplifying 2 exons in a conserved domain and their intervening  
CC intron. The human p53 gene was localised to chromosomal position  
CC 3q27-29. At least 6 different isoforms exist. Splice variants  
CC differing at the C-terminus have been designated as alpha, beta and  
CC gamma forms, while p63 members differing in the N-terminus are  
CC designated as delta and TA forms, where the delta form lacks the  
CC transactivation domain. The present sequence represents human  
CC p63 isotype Tap63 beta. p63 was detected in a variety of  
CC human and mouse tissue. It demonstrates remarkably divergent  
CC activities, such as the ability to transactivate p53 reporter genes  
CC and induce apoptosis. Cessation or down-regulation of p63 expression  
CC may play a critical role in the process of cervical squamous  
CC differentiation, both benign and neoplastic. Delta isoforms of p63  
CC act as dominant negatives towards transactivation by p53 and p63.  
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.  
CC cachexia) and neuronal differentiation and related degenerative  
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see  
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to  
CC identify compounds useful for treating disorders involving such  
CC processes, in detection and diagnosis, and in the production of  
CC transgenic animals.

XX Sequence 516 AA;

Query Match 91.7%; Score 2185; DB 20; Length 516;

Best Local Similarity 94.1%; Pred. No. 2.2e-189;

Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDINFVDESEDAATNKIEISMDCIIMQ 60  
DB 1 msqstqetneflspsvfgqhlwdfleqplcsvqpldlnfvdpsengatnkietmdclmq 60



```

OY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 dsdlsdpmpqytnlglnsmdqoiongssstspynldhagnsvtapsyaqpsstfdal 120
OY 121 SPSPALPSNTDYPGPHSFDVSPQOOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 spspalpsntdygphsfdvsfqgsstaksatwtstlkklyqiaktcpdqikvmttpp 180
OY 181 POGAVIRAMPYVYKKAHVTEVVKRCPNHLELSREFNEGOIAPPSHLIVEGNSHAQYVEDP 240
DB 181 ppgavirampvykkaehvtevkrcpnhelelsrefneqiappshllivegnshaqyvedp 240
OY 241 ITGKQSVLVYEPPOVTEFTTVLYNFMCMSSCYGMMRRPILITVLERDGOVLCRRC 300
DB 241 itgrqsvlvypvpepvgteftvlynmcmsscvgmmrrpiliivlelctrdgvgvlgrc 300
OY 301 FEARICACPGRRKADDSIRKQOVSDSTKNGDGTKRPPRONTHTGIOMTSIKRRSPDDE 360
DB 301 fearicacpgrrdkadedsirkgvdsstkngdgtkrpfrqntngtqmtsikrrspdde 360
OY 361 LLYLPVGRRETYEMLKIKESLEIMQYLPQHTTETTYRQOQOQOHHLLQKHLISACFRNE 420
DB 361 llylpvgrretyemllkikeslelmqylpqhtletyrgqgqgqnhllqk----- 410
OY 421 LVEPRRETPOKSDVFRHSKRP 442
DB 421 -----qtsiqspssygnssp 426

```

## RESULT 6

AAB11363  
ID AAB11363 standard; Protein; 516 AA.

AC AAB11363;

DT 21-FEB-2001 (first entry)

DE Human p53 protein isoform #7.

KW Lung cancer: therapy; treatment; human; tumor; immunogenic; cytostatic;

KM vaccine; detection.

OS Homo sapiens.

PN WO200061612-A2.

PD 19-OCT-2000.

PF 03-APR-2000; 2000MO-0508896.

PR 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

XX (COR-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI; 2000-628399/60.

XX N-PSDB; AAC66033.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor

XX protein is used for detecting and monitoring progression of lung cancer

XX in a patient -

XX Disclosure; Page 255-256; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which

XX comprising an immunogenic portion of a lung tumor protein or variant (P2)

XX which have cytostatic activity. The polypeptides and polynucleotides are

CC used in compositions and vaccines to inhibit the development of cancer,  
CC especially lung cancer, in a patient. Methods described in the invention  
CC can be used to monitor the progression of a cancer by carrying out the  
CC detection at subsequent time points and comparing the results from the  
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient  
CC are treated with P2, polynucleotides encoding P2 or antigen presenting  
CC cells expressing P2 and then administered to the patient to inhibit  
CC development of cancer.

XX Sequence 516 AA:

Query Match 91.7%; Score 2185; DB 21; Length 516;  
Best Local Similarity 94.1%; Pred. No. 2.2e-189;  
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```

OY 1 MSOSTQTNELSPVEFQHIWDFLEQIPICSVQPIDLNFVDEPSEDEGATNKKIEMDCIRMQ 60
DB 1 msqstqtnelfspvefqhiwdfleqpicsvqpidlnfvdesedgatnkkiemdcirmq 60
OY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 dsdlsdpmpqytnlglnsmdqoiongssstspynldhagnsvtapsyaqpsstfdal 120
OY 121 SPSPALPSNTDYPGPHSFDVSPQOOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 spspalpsntdygphsfdvsfqgsstaksatwtstlkklyqiaktcpdqikvmttpp 180
OY 181 POGAVIRAMPYVYKKAHVTEVVKRCPNHLELSREFNEGOIAPPSHLIVEGNSHAQYVEDP 240
DB 181 ppgavirampvykkaehvtevkrcpnhelelsrefneqiappshllivegnshaqyvedp 240
OY 241 ITGKQSVLVYEPPOVTEFTTVLYNFMCMSSCYGMMRRPILITVLERDGOVLCRRC 300
DB 241 itgrqsvlvypvpepvgteftvlynmcmsscvgmmrrpiliivlelctrdgvgvlgrc 300
OY 301 FEARICACPGRRKADDSIRKQOVSDSTKNGDGTKRPPRONTHTGIOMTSIKRRSPDDE 360
DB 301 fearicacpgrrdkadedsirkgvdsstkngdgtkrpfrqntngtqmtsikrrspdde 360
OY 361 LLYLPVGRRETYEMLKIKESLEIMQYLPQHTTETTYRQOQOQOHHLLQKHLISACFRNE 420
DB 361 llylpvgrretyemllkikeslelmqylpqhtletyrgqgqgqnhllqk----- 410
OY 421 LVEPRRETPOKSDVFRHSKRP 442
DB 421 -----qtsiqspssygnssp 426

```

## RESULT 7

AAV45247  
ID AAV45247 standard; Protein; 641 AA.

AC AAV45247;

DT 07-JAN-2000 (first entry)

DE Human p51 protein B.

KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;

KM tumour suppression; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Domain 1..59 /label= transactivation\_domain

XX Domain 142..321 /label= DNA\_binding\_domain

XX Domain 353..397 /label= oligomerisation\_domain

XX WO950412-A1.



```

Oy 61 DSDLSDDPMWPTYNLIGLINSMDOO IONGSSSTSPYNDHONSTVAPSAOOSPFDAI 120
Db 61 dsdlsddpmwptynlignsmdoo iongssstspyndhons tvapsaoospfda i120
Oy 121 SPSPAIPSNIDYPCGPHSFDVSFOQSSSTAKSATWYSTELKILYCOLIKTCRPIQIKWTP 180
Db 121 spspaipsnidypcgphsfdvsfoqssstak satwystelkilycoliktc rpiqikwtp 180
Oy 121 spspaipsnidypcgphsfdvsfoqssstak satwystelkilycoliktc rpiqikwtp 180
Db 121 spspaipsnidypcgphsfdvsfoqssstak satwystelkilycoliktc rpiqikwtp 180
Oy 181 PGCAVIRAMPYKKAENVTEYVKRCRPHHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
Db 181 pgcavirampykkaenvteyvkrcrphhe lsrefnegqiappshlirve gnsahayedp 240
Oy 241 ITGROSUVLVRPERPQVCTSEETTVLYNMCMSGCCGNNRRRRLILYTLERDQOVLGRRC 300
Db 241 itgrosuvlvrperpqvctseetvlynmc msccgnnrrrrlilytler dqovlgrrc 300
Oy 301 FEARICACPGHRKADADSDIRKOOVSDSTKNGDSTRKPRFQNTNGIOMTISIKRRSPDDE 360
Db 301 fearicacpghrkadadsdirkoo vsdstkn gdstkrprfqntngiomt isikrrspdde 360
Oy 361 LLYLVRKRETYEMLLIKESLELMQYLPHNTLETYKQOQOQOQHLLQKNLLSACFRNE 420
Db 361 llylvrkretyemllikeslelmqylph ntletykqoqoqoqhllqknllsacfrne 420
Oy 421 LVRPRRETPKQSDVFRNKSRR 442
Db 421 -----qsdspssygnsspp 426

```

CC especially lung cancer. In a patient. Methods described in the invention  
CC can be used to monitor the progression of a cancer by carrying out the  
CC detection at subsequent time points and comparing the results from the  
CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient  
CC are treated with P2, polynucleotides encoding P2 or antigen presenting  
CC cells expressing P2 and then administered to the patient to inhibit  
CC development of cancer.



Db 340 fearlaccpgrdrkadedsirkqvsdskngdglkprfgrnltnglqmtsikrrspdde 399  
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOOHOLLOKHLILSACFENE 420  
 Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQGGQGHLLQK----- 449  
 QY 421 LVEPRRETPKOSDVFFRHSKRP 442  
 Db 450 -----qtsiqspssysgnsspp 465  
 RESULT 12  
 AAY05958  
 ID AAY05958 standard; Protein; 680 AA.  
 AC AAY05958;  
 DT 16-AUG-1999 (first entry)  
 DE Human cell regulatory protein p63, isoform deltaNp63 gamma.  
 XX Cell regulatory protein: p63; hu-deltaNp63 gamma; human;  
 KM cancer; tumour suppressor; cell cycle control; apoptosis;  
 KM cell proliferation; cell differentiation; therapy.  
 OS Homo sapiens.  
 XX MO9919357-A2.  
 PN 22-APR-1999.  
 XX 02-OCT-1998; 98MO-US21992.  
 PE 29-MAY-1998; 98US-0087216.  
 PR 15-OCT-1997; 97US-0062076.  
 XX (HARD ) HARVARD COLLEGE.  
 PA MCKEON F, Yang A;  
 PI WPI; 1999-277595/23.  
 DR N-PSDB; AAX58577.  
 XX New isolated p63 cell regulatory protein for, e.g. treatment of  
 PT tumours  
 PS Claim 23; Fig 14; 161pp; English.  
 XX The present invention concerns the discovery of a new family of  
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,  
 CC which demonstrate certain sequence identity to known tumour  
 CC suppressor proteins p53 and p73. It has been observed that the  
 CC intron-exon organisation is conserved between p73 and p53, and from  
 CC known exon and intron sizes for these 2 genes, it was possible to  
 CC identify new members of this gene family using a PCR-based strategy  
 CC of amplifying 2 exons in a conserved domain and their intervening  
 CC intron. The human p53 gene was localised to chromosomal position  
 CC 3q27-29. At least 6 different isoforms exist. Splice variants  
 CC differing at the C-terminus have been designated as alpha, beta and  
 CC gamma forms, while p63 members differing in the N-terminus are  
 CC designated as delta and TA forms, where the delta form lacks the  
 CC transactivation domain. The present sequence represents human  
 CC p63 isoform hu-deltaNp63 gamma. p63 was detected in a variety  
 CC of human and mouse tissue. It demonstrates remarkably divergent  
 CC activities, such as the ability to transactivate p53 reporter genes  
 CC and induce apoptosis. Cessation or down-regulation of p63 expression  
 CC may play a critical role in the process of cervical squamous  
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63  
 CC act as dominant negatives towards transactivation by p53 and p63.  
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.  
 CC cachexia) and neuronal differentiation and related degenerative  
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see  
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to

CC identify compounds useful for treating disorders involving such  
 CC processes, in detection and diagnosis, and in the production of  
 CC transgenic animals.  
 CC XX  
 S0 Sequence 680 AA;  
 Query Match 91.0%; Score 2169; DB 20; Length 680;  
 Best Local Similarity 93.2%; Pred. No. 9,3e-188;  
 Matches 412; Conservative 6; Mismatches 8; Indels 16; Gaps 1;  
 QY 1 MSQSTQTNFELSPVEYGHIMDFLEDPICSYOPIDUNFVDEPSEDGATNKIEISMDICRMQ 60  
 Db 40 msgstqtselispvefghlwdlqpicvqplanfvdpsenganklelsmndclmq 99  
 QY 61 DSDLSDFPMPOYTNGULNSMDQOIQNGSSSTSPYNDHAQNSTAPSPYAQPSSTFDAL 120  
 Db 100 dsdlsdfpmppqytnlglnsmndqqlngssstspynlthagnsvlapspyqpsstfda 159  
 QY 121 SPSPAIPSENTDYPGPHSFDFVSFOOSSTPAKSATWTYSTFLKLYCOIAKTCPIQKVMTPP 180  
 Db 160 spspaispntdypgphsfdfvsfqsstakstwtystelklycqiaktcpqlkvmtp 219  
 QY 181 PGAVIRAMPYKKAHEHYTEVYKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYEDP 240  
 Db 220 pgavirampykkahelvkrpcphelshrefnegqlappshlirvegnshaqyedp 279  
 QY 241 ITGRQSVLYPREPQVYGFETTVLYXNFMCNSSCYGAMRRPILITVLETDGQVLAGRC 300  
 Db 280 itgrqsvlyprepvygfetvlylnfmcnsscygammrrpilitvletdgvlagrc 339  
 QY 301 FEARICACPRGRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIOWTSIKRRSPDPE 360  
 Db 340 fearlaccpgrdrkadedsirkqvsdskngdglkprfgrnltnglqmtsikrrspdde 399  
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOOHOLLOKHLILSACFENE 420  
 Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQGGQGHLLQK----- 449  
 QY 421 LVEPRRETPKOSDVFFRHSKRP 442  
 Db 450 -----qtsmqsgssysgnsspp 465  
 RESULT 13  
 ID AAY05998 standard; Protein; 680 AA.  
 AC AAY05998;  
 DT 14-MAR-2000 (first entry)  
 DE Rat KET protein.  
 XX Rat KET protein.  
 KM KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;  
 KM p53 family; angiogenic; cytotoxic; cancer; rat.  
 OS Rattus sp.  
 XX WO9961610-A2.  
 PN 02-DEC-1999.  
 PD 25-MAY-1999; 99WO-DE01557.  
 PE 25-MAY-1998; 98DE-1022985.  
 PR (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.  
 PA Paul D, Augustin M, Schmale H, Bamberger C;  
 PI WPI; 2000-062710/05.  
 DR



```

|||||
Db 195 pyppqygleftvlylhmcmsscvgmmrrp1llivletrdqvlgrrcfearicacp 254
OY 310 GRDRKADSDSIRKQOVSDSTKNGDGTKRPFONTHGIOMTSIKRRSRDDELLYLPVGR 369
Db 255 grdrkadeadsirkqvsostakngdgtkrpfrngthgimtsikrrspddellylpvgr 314
OY 370 ETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLLQKHLISACPRNELVPERRET 429
Db 315 etyemllkikeslelmqylpqhtietryrqgqgqbhl1qchllsacrfnelvperretp 374
OY 430 KQSDVFRHRSKPPNRSYVP 448
Db 375 kgsdvfrhskppnrsvyp 393

RESULT 15
AAI05964
ID AAY05964 standard; protein; 389 AA.
AC AAY05964;
XX
XX 16-AUG-1999 (first entry)
DT
XX
XX Mouse cell regulatory protein p63, isoform delta1p63 gamma, cDNA.
DE
XX
XX Cell regulatory protein: p63; mu-delta1p63 gamma; mouse:
KM cancer; tumour suppressor; cell cycle control; apoptosis;
KM cell proliferation; cell differentiation; therapy.
XX
XX Mus sp.
OS
XX
XX MO9919357-A2.
PN
XX
XX 22-APR-1999.
PD
XX
XX 02-OCT-1998; 98MO-US21992.
PF
XX
XX 29-MAY-1998; 98US-0087216.
PR
PR 15-OCT-1997; 97US-0062076.
XX
XX (HARD ) HARVARD COLLEGE.
PA
XX
XX McKeon F, Yang A;
PI
XX
XX WPI: 1999-277595/23.
DR
DR N-PSDB; AAX58583.
XX
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
XX
XX Claim 23: Fig 20: 161pp; English.
XX
XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
CC amplified cDNA possessed a truncated N-terminus, i.e. the
CC transactivation domain was absent. Additional splice variants were
CC identified by screening a cDNA library with a probe corresponding
CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
CC variants differing at the C-terminus are designated as alpha, beta
CC and gamma forms, while p63 members differing in the N-terminus are
CC designated as delta1 and TA forms, where the delta1 form lacks the
CC transactivation domain. The present sequence represents mouse p63
CC isoform mu-delta1p63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta1 isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.

```

```

CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
XX
SQ Sequence 389 AA;
Query Match 81.3%; Score 1938; DB 20; Length 389;
Best Local Similarity 97.1%; Pred. No. 3,5e-167;
Matches 368; Conservative 0; Mismatches 7; Indels 4; Gaps 1;
OY 70 PQTNLGLNLSMDOOIQNGSSSTSPYNTDHAQNSTAPYAQPSFTDALSPAPISN 129
Db 15 pytnlglnlsmddq1qngssstspyntdhaqnsvtapsyapqstldalspsalpsn 74
OY 130 TDYGPBHSFDVSPFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVTPPPGAVIRAM 189
Db 75 tdypghsfdivsfqgstaksatwtystelkklycqjaktcpiqikvtpppgaviram 134
OY 190 PYYKKAHEVTEYVKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQYVEDITGROSVLV 249
Db 135 pykkaehvtevkrcpnhelsrefneq1appshlirvegnshaqyveditgrsvlv 194
OY 250 PYEPPQVTEFTTYLYINMCNSSCYCGMNRRLIYVLETRDQVLCGRCFEARIACCP 309
Db 195 pyppqygleftvlylhmcmsscvgmmrrp1llivletrdqvlgrrcfearicacp 254
OY 310 GRDRKADSDSIRKQOVSDSTKNGDGTKRPFONTHGIOMTSIKRRSRDDELLYLPVGR 369
Db 255 grdrkadeadsirkqvsostakngdgtkrpfrngthgimtsikrrspddellylpvgr 310
OY 370 ETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLLQKHLISACPRNELVPERRET 429
Db 311 etyemllkikeslelmqylpqhtietryrqgqgqbhl1qchllsacrfnelvperretp 370
OY 430 KQSDVFRHRSKPPNRSYVP 448
Db 371 kgsdvfrhskppnrsvyp 389

```

Search completed: August 8, 2001, 01:35:36  
Job time: 4872 sec

---



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 8, 2001, 00:15:39 ; Search time 57.45 Seconds  
(Without alignments)  
160,565 Million cell updates/sec

Title: US-09-670-568B-1

Perfect score: 2383  
Sequence: 1 MSQSTQTEFLSPVFQHTW.....PKQSDVFRHSPKPRNSYYP 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA :  
1: /cgnl\_7/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgnl\_7/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgnl\_7/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgnl\_7/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgnl\_7/ptodata/1/1aa/PTUS.COMB.pep.\*  
6: /cgnl\_7/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	722.5	30.3	393	1 US-08-047-041A-27	Sequence 27, Appl
2	722.5	30.3	393	1 US-08-390-516C-8	Sequence 8, Appl
3	722.5	30.3	393	1 US-08-390-515A-8	Sequence 8, Appl
4	722.5	30.3	393	2 US-08-801-718-8	Sequence 8, Appl
5	717.5	30.1	363	2 US-08-697-221-17	Sequence 17, Appl
6	717.5	30.1	393	1 US-08-047-041A-25	Sequence 25, Appl
7	717.5	30.1	393	1 US-08-047-041A-26	Sequence 26, Appl
8	717.5	30.1	393	1 US-08-347-792-2	Sequence 2, Appl
9	717.5	30.1	393	1 US-08-390-516C-6	Sequence 6, Appl
10	717.5	30.1	393	1 US-08-431-357-2	Sequence 2, Appl
11	717.5	30.1	393	1 US-08-390-515A-6	Sequence 6, Appl
12	717.5	30.1	393	1 US-08-380-515A-7	Sequence 7, Appl
13	717.5	30.1	393	1 US-08-380-515A-7	Sequence 7, Appl
14	717.5	30.1	393	2 US-08-795-006A-32	Sequence 32, Appl
15	717.5	30.1	393	2 US-08-697-221-2	Sequence 2, Appl
16	717.5	30.1	393	2 US-08-801-718-6	Sequence 6, Appl
17	717.5	30.1	393	2 US-08-801-718-7	Sequence 7, Appl
18	717.5	30.1	393	3 US-08-247-904B-12	Sequence 12, Appl
19	717.5	30.1	393	3 US-08-767-942A-23	Sequence 23, Appl
20	717.5	30.1	393	4 US-08-352-542-2	Sequence 2, Appl
21	717.5	30.1	393	4 US-09-184-073-32	Sequence 32, Appl
22	717.5	30.1	393	4 US-08-328-673A-9	Sequence 9, Appl
23	717.5	30.1	393	4 US-08-894-327-2	Sequence 2, Appl
24	717.5	30.1	439	5 PCT-US95-15353-2	Sequence 2, Appl
25	717.5	30.1	439	2 US-08-959-638-9	Sequence 9, Appl
26	716.5	30.1	363	2 US-08-697-221-18	Sequence 18, Appl
27	716.5	30.1	393	1 US-08-047-041A-28	Sequence 28, Appl

## ALIGNMENTS

28	716.5	30.1	393	1 US-08-390-516C-9	Sequence 9, Appl
29	716.5	30.1	393	1 US-08-390-515A-9	Sequence 9, Appl
30	716.5	30.1	393	2 US-08-697-221-3	Sequence 3, Appl
31	716.5	30.1	393	2 US-08-697-221-4	Sequence 4, Appl
32	716.5	30.1	393	2 US-08-801-718-9	Sequence 9, Appl
33	716.5	30.1	393	2 US-08-675-631-1	Sequence 1, Appl
34	713.5	29.9	363	2 US-08-697-221-19	Sequence 19, Appl
35	713.5	29.9	393	2 US-08-697-221-11	Sequence 11, Appl
36	712.5	29.9	363	2 US-08-697-221-20	Sequence 20, Appl
37	712.5	29.9	363	2 US-08-697-221-21	Sequence 21, Appl
38	712.5	29.9	393	2 US-08-697-221-12	Sequence 12, Appl
39	712.5	29.9	393	2 US-08-697-221-14	Sequence 14, Appl
40	712.5	29.9	393	2 US-08-697-221-25	Sequence 25, Appl
41	711.5	29.9	363	2 US-08-697-221-22	Sequence 22, Appl
42	711.5	29.9	393	2 US-08-697-221-15	Sequence 15, Appl
43	711.5	29.9	393	2 US-08-697-221-27	Sequence 27, Appl
44	711	29.8	390	1 US-08-347-792-15	Sequence 15, Appl
45	711	29.8	390	1 US-08-431-357-15	Sequence 15, Appl

RESULT 1  
US-08-047-041A-27  
Sequence 27, Application US/08047041A  
Patent No. 5527676  
GENERAL INFORMATION:  
APPLICANT: Vogelstein, Bert  
APPLICANT: Baker, Suzanne J.  
APPLICANT: Fearon, Eric R.  
APPLICANT: Nigro, Janice M.  
TITLE OF INVENTION: Detection of Loss of the Wild-Type p53  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001.4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/047, 041A  
FILING DATE: 22-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/928, 661  
FILING DATE: 17-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/446, 584  
FILING DATE: 06-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/330, 566  
FILING DATE: 29-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42917  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 393 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 PUBLICATION INFORMATION:  
 AUTHORS: Harris, et al.,  
 JOURNAL: Mol. Cell. Biol.  
 VOLUME: 6  
 ISSUE: 12  
 PAGES: 4650-4656  
 DATE: 1986  
 US-08-047-041A-27

Query Match 30.3%; Score 722.5; DB 1; Length 393;  
 Best Local Similarity 40.5%; Pred. No. 1.2e-60;  
 Matches 155; Conservative 57; Mismatches 116; Indels 55; Gaps 7;

QY 11 LSPVFOHIMDFEOPICSVQPIDLNFVDEPSEDEGATNKIEISMDICIMODSDLSDEMPMP 70  
 DB 14 LSGEFTSDLMKLLPE-----NNVLSPLPSQAMDDMLSPDDIEQWTE--DP--- 58  
 QY 71 QYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQSPSTFDALSPSPA----- 125  
 DB 59 -----GPDAPRMPEAPPAVAPATPTPPAPAPAPASWPL 93  
 QY 126 ---IPSNTRYDGPSPHSDVFOOSSTAKSATWTYSTELKLYQIAKTCPIQIKWTPPPQ 182  
 DB 94 SSSVPSQKTYGSGYGRGLGFLHSGTAKSVCTYSPALNKMFCQIAKCPQVLWVDSPP 153  
 QY 183 GAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPIT 242  
 DB 154 GTRVRAMALYKXOSHMTEVVRCPHNE--RCSDSGLAPQHLIRVEGNLRVEYLDDBRT 211  
 QY 243 GROSVLVPEPPOVGTETTYLYNFCNSSCGVMNRPLILITVLETRDGOVLRGRCFE 302  
 DB 212 FRHSVVPYEPPEVSGDCTTIHYNYMCNSSCGVMNRPLITITLEDSSGNLGRNSE 271  
 QY 303 ARICACPRDKKADEDSIRKQVSDSTKNGDGTKRPRFRONTGHIQWTSIKRRSP--DDEL 361  
 DB 272 VRVACACPRDRRTEENLRKGPHEHLPRGSTKRALPNNT-----SSSPQPKKKPLDGEY 327  
 QY 362 LYLPRGRETETMLKIKESLEL 384  
 DB 328 FTLOIRGREREMFRELNEALEL 350

RESULT 2  
 US-08-390-516C-8  
 Sequence 8, Application US/08390516C  
 Patent No. 5708136  
 GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILEE  
 APPLICANT: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 STREET: 1001 G STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20001  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/390,516C

FILING DATE: 07-APR-1993  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107,42798  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9100  
 TELEFAX: 202-508-9299  
 TELETYPE: 197430 BMBB UT  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 393 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 PUBLICATION INFORMATION:  
 AUTHORS: Harris, et al.,  
 JOURNAL: Mol. Cell. Biol.  
 VOLUME: 6  
 ISSUE: 12  
 PAGES: 4650-4656  
 DATE: 1986  
 US-08-390-516C-8

Query Match 30.3%; Score 722.5; DB 1; Length 393;  
 Best Local Similarity 40.5%; Pred. No. 1.2e-60;  
 Matches 155; Conservative 57; Mismatches 116; Indels 55; Gaps 7;

QY 11 LSPVFOHIMDFEOPICSVQPIDLNFVDEPSEDEGATNKIEISMDICIMODSDLSDEMPMP 70  
 DB 14 LSGEFTSDLMKLLPE-----NNVLSPLPSQAMDDMLSPDDIEQWTE--DP--- 58  
 QY 71 QYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQSPSTFDALSPSPA----- 125  
 DB 59 -----GPDAPRMPEAPPAVAPATPTPPAPAPAPASWPL 93  
 QY 126 ---IPSNTRYDGPSPHSDVFOOSSTAKSATWTYSTELKLYQIAKTCPIQIKWTPPPQ 182  
 DB 94 SSSVPSQKTYGSGYGRGLGFLHSGTAKSVCTYSPALNKMFCQIAKCPQVLWVDSPP 153  
 QY 183 GAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPIT 242  
 DB 154 GTRVRAMALYKXOSHMTEVVRCPHNE--RCSDSGLAPQHLIRVEGNLRVEYLDDBRT 211  
 QY 243 GROSVLVPEPPOVGTETTYLYNFCNSSCGVMNRPLILITVLETRDGOVLRGRCFE 302  
 DB 212 FRHSVVPYEPPEVSGDCTTIHYNYMCNSSCGVMNRPLITITLEDSSGNLGRNSE 271  
 QY 303 ARICACPRDKKADEDSIRKQVSDSTKNGDGTKRPRFRONTGHIQWTSIKRRSP--DDEL 361  
 DB 272 VRVACACPRDRRTEENLRKGPHEHLPRGSTKRALPNNT-----SSSPQPKKKPLDGEY 327  
 QY 362 LYLPRGRETETMLKIKESLEL 384  
 DB 328 FTLOIRGREREMFRELNEALEL 350

RESULT 3  
 US-08-390-515A-8  
 Sequence 8, Application US/08390515A  
 Patent No. 5756455  
 GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILEE  
 APPLICANT: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,515A  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEO ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 393 amino acids  
TYPE: amino acid  
MOLECULE TYPE: linear  
HYPOTHEICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Harris, et al.,  
JOURNAL: Mol. Cell. Biol.  
VOLUME: 6  
ISSUE: 12  
PAGES: 4650-4656  
DATE: 1986  
US-08-390-515A-8

Query Match 30.3%; Score 722.5; DB 1; Length 393;  
Best Local Similarity 40.5%; Pred. No. 1.2e-60;  
Matches 155; Conservative 57; Mismatches 116; Indels 55; Gaps 7;

QY 11 LSPFVQIHNDLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQDSLDSDMP 70  
DB 14 LSOETFSIDLKLP-----NNVLSPLPSQAMDILMSDDIEQWTE--DP--- 58  
QY 71 QYTNLGLINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA----- 125  
DB 59 -----GPDEAPRMPEAPPVAPATPTPAAPAPAPSPML 93  
QY 126 ---IPSTNDYRGHSPDVSFOQSTASTATYTYSTELKLYCQIAKCPIDIKMTTPPQ 182  
DB 94 SSSVPSQKTYQSGTFLGSLHSTAKSVCTYSPALNKMFCQIAKCPYQWLWVDSSTPP 153  
QY 183 GAVIRAPVYKKAHEVYKRCPNHLSREFNCGOIAPSHLIRVGNASHAQVVEPIT 242  
DB 154 GTRVRAAIIKQSOHMEVYKRCPHNE--RCSDSDGLAPQHLIRVGNLREVELDTRNT 211  
QY 243 GROSIVLPPVPPVQTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLRGCFE 302  
DB 212 FRHSVYVYPPPEVGSCTIITHYVMCNSSCMGMNRRPILITITLDDSGNLLGRSFE 271  
QY 303 ARICACGRKAKADESIRKQOVSSTKNGDGTRKPRONTHTGIQTSIKKRSP-DDEL 361  
DB 272 VRVACGGRDRRTTEENLRKKRGPHEHLPQSTKRALPNNT---SSSPQPKKKPLDGEY 327

QY 362 LYLPVGRRETYEMLKIKESLEL 384  
DB 328 FTLOIRGRERFERMELENALEL 350

RESULT 4  
US-08-801-718-8  
Sequence 8, Application US/08801718  
Patent No. 5858976  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
NUMBER OF SEQUENCES: 9  
TITLE OF INVENTION: HUMAN TUMORS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,718  
FILING DATE: 14-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,515  
FILING DATE: 07-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEO ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 393 amino acids  
TYPE: amino acid  
MOLECULE TYPE: linear  
HYPOTHEICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Harris, et al.,  
JOURNAL: Mol. Cell. Biol.  
VOLUME: 6  
ISSUE: 12  
PAGES: 4650-4656  
DATE: 1986  
US-08-801-718-8

Query Match 30.3%; Score 722.5; DB 2; Length 393;  
Best Local Similarity 40.5%; Pred. No. 1.2e-60;  
Matches 155; Conservative 57; Mismatches 116; Indels 55; Gaps 7;

QY 11 LSPFVQIHNDLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQDSLDSDMP 70  
DB 14 LSOETFSIDLKLP-----NNVLSPLPSQAMDILMSDDIEQWTE--DP--- 58

[illegible]

```

1      RESULT 5
2      US-08-697-221-17
3      Sequence 17, Application US/08697221
4      Patent No 5847083
5      GENERAL INFORMATION:
6      APPLICANT: Halaconetis, Thanos D.
7      TITLE OF INVENTION: Modified p53 Constructs and
8      TITLE OF INVENTION: Therefore
9      NUMBER OF SEQUENCES: 33
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Howson and Howson
12     STREET: Spring House Corporate Cntr., PO Box 4
13     CITY: Spring House
14     STATE: Pennsylvania
15     COUNTRY: USA
16     ZIP: 19477
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: Patent Release #1.0, Version #1.30
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/08/697,221
24     FILING DATE:
25     CLASSIFICATION: 530
26     PRIOR APPLICATION DATA:
27     APPLICATION NUMBER: US 60/004,802
28     FILING DATE: 22-SEP-1995
29     ATTORNEY/AGENT INFORMATION:
30     NAME: Kodroff, Cathy A.
31     REGISTRATION NUMBER: 33,980
32     REFERENCE/DOCKET NUMBER: WST64AUSA
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: 215-540-9206
35     TELEFAX: 215-540-5818
36     INFORMATION FOR SEQ ID NO: 17:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 363 amino acids
39     TYPE: amino acid
40     STRANDEDNESS:
41     TOPOLOGY: linear
42     MOLECULE TYPE: protein
43     US-08-697-221-17

```

Query Match	30.1%;	Score 717.5;	DB 2;	Length 363;
Best Local Similarity	39.7%;	Pred. No. 3.1e-60;		
Matches 156;	Conservative 60;	Mismatches 102;	Indels 75;	Gaps 11;

```

0Y 11 LSPBYFQIHWDLQ-----PICS-----VQPIDLN--FVDEPSEDGATNKIEISMD 56
Db 14 LSOEFTFSDLMKLLPBNVNLSPLSQAMDLMLSPDIIQFQWTEPBGDEA----- 63
0Y 57 IRMODSDLSDDPMAPYTNLGIILNSMDQIQNGSSSTSYNNDHQNSTAPSPAQSSST 116
Db 64 -----PMME-----:-----AAP-----VAPAP-AAETPA 83
0Y 117 FDALSP-----SPALSPNIDYDGPBHSFDVSPFOSSSTAKATWTYTELKLCOJAKTCPI 172
Db 84 AAPAPSPWBLSSVPSQKTOGSGYGFRLGFLHSIGAKSVTCTYPALNKMPCQJAKTCPV 143
0Y 173 QIKWNTPPQCAVIRAMVYVYKAEHYTEVYKRCPNHLSRENEGQIAPSPHLIRVEGNS 233
Db 144 QIWDVSTPPRGVRVAMAIYKOSOHMEVYRCPHNE--RCSDDGLAPPHLIRVEGNL 201
0Y 233 HAOYVEDPITGROSIVLYEPPVOGTETFTVLNPMCNSSCVGGMNRRPILIIYLETBD 292
Db 202 RVEYIDNDKNTFRHSVYVYEPPEVGSDDTIIHNYMNCSSCGMMNRRPILIIYLETDS 261
0Y 293 GOVIGRRCFEARICACPRDKRADEDSIRKQOYDSTKNGDGTKRPRQNTHTGIOMTSIK 352
Db 262 GNLLGRNFSFEVRYVACAPGRDRTDEENLRKKGBRHHELPGSTKRALPNNT-----SSPQ 317
0Y 353 KRSP--DDELLLYPRGBREYEMLKIKESLET 384
Db 318 PKKKPFOEYFTTQIQIRGREREMRELNEALET 350

```

RESULT 6  
 US-08-047-041A-25  
 : Sequence 25, Application US/08047041A  
 Patent No. 5527676  
 GENERAL INFORMATION:  
 APPLICANT: Vogelstein, Bert  
 APPLICANT: Baker, Suzanne J.  
 APPLICANT: Fearon, Eric R.  
 APPLICANT: Nigro, Janice M.  
 TITLE OF INVENTION: Detection of Loss of the wild-type p53  
 TITLE OF INVENTION: Gene  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Banner & Allegretti, Ltd.  
 STREET: 1001 G Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20001.4597  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/047.041A  
 FILING DATE: 22-MAR-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/928,661  
 FILING DATE: 17-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/446,584  
 FILING DATE: 06-DEC-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/330,566  
 FILING DATE: 29-MAR-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kagan, Sarah A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107.42917  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9100



Db 332 IRGRERFEMFELNEALEL 350

## RESULT 8

US-08-347-792-2

Sequence 2, Application US/08347792  
Patent No. 5573925

## GENERAL INFORMATION:

APPLICANT: Halazonetis, Thanos D.

TITLE OF INVENTION: p53 Proteins With Altered

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr., PO Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/347,792

APPLICATION NUMBER: US/08/347,792

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST580USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 393 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-347-792-2

Query Match 30.1%; Score 717.5; DB 1; Length 393;  
Best Local Similarity 39.7%; Pred. No. 3.5e-60;

Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

11 LSPVEFOHIMDFLEQ-----PICS-----VOPIDLN--FVDEPSEDGATNKIEISMDC 56

14 LSOETFSIDLKLPENNVLSPQAMDMLSPDDIEQWFTEDPGPDEA----- 63

57 IRMODSDLSDPMPQYTNLGLINSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAPSPST 116

64 -----PRMPE-----AAP-----VAPAP-AAFTPA 83

117 FDALSP-----SPAISSNDYDGPSPHSDVSPFOOSSTAKSATWTYSTELKLYCOIAKTCP 172

84 APAPAPSPPLSSVPSOKTTOGSGFRGLHSGTAKSVCTYCTSPALNKKMFCOLAKTCPV 143

173 QIKVMTTPPOGAVIRAMPVYKKAHVTEVVKRCPNHELSEEFNNGOIAAPSHLIRVGN 232

144 QLVAVDSPPPTGTRVRAIAIKQSQHMEVVRRCRCHNE--KCSBDSGLAPQOHLIRVEGNL 201

233 HAQVDEPIRGROSLVLYPERPOVGETFTVLYNFCMNSSCVGMMNRPIILITVLETRD 292

202 RVEVLDRNFRHSVVVYPERPEVSGDCTIHYNYMNCSSCMGMNRPILITITLEDSS 261

293 GVLGRSCFEARICACPGRRKKADESDIRKOQVSDSTKNGDGKRRPROMTHIQMTSIK 352

262 GNLLGRNSFEVRVACACGRDRKTEENLRKKGEHHELPFGSTKRALPNNT-----SSSPQ 317

QY 353 KRSP-DDELLYPRGRETVELKIKESIEL 384  
Db 318 PKKKPLDGEYFTLQIRGRERFEMFELNEALEL 350

## RESULT 9

US-08-390-516C-6

Sequence 6, Application US/08390516C  
Patent No. 5708136

## GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE

APPLICANT: HILL, DAVID E.

APPLICANT: KINZLER, KENNETH W.

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/390,516C

APPLICATION NUMBER: US/08/390,516C

FILING DATE: 07-APR-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107,42798

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 393 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOHETICAL: YES

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

AUTHORS: Buchanan, et al.,

JOURNAL: Gene

VOLUME: 70

PAGES: 245-252

DATE: 1988

US-08-390-516C-6

Query Match

30.1%; Score 717.5; DB 1; Length 393;  
Best Local Similarity 39.7%; Pred. No. 3.5e-60;

Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

11 LSPVEFOHIMDFLEQ-----PICS-----VOPIDLN--FVDEPSEDGATNKIEISMDC 56

14 LSOETFSIDLKLPENNVLSPQAMDMLSPDDIEQWFTEDPGPDEA----- 63

57 IRMODSDLSDPMPQYTNLGLINSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAPSPST 116

64 -----PRMPE-----AAP-----VAPAP-AAFTPA 83

117 FDALSP-----SPAISSNDYDGPSPHSDVSPFOOSSTAKSATWTYSTELKLYCOIAKTCP 172

Db 84 AAPAPSMPLSSSVPSQKTYGSGYFRLGFLHSGTAKSVCTCTSPALNKKMFCQIAKTCPV 143  
QY 173 QIKVMTPPGQAVIRAMPYKKAHVTYVKKCPNHELSEFNEGQIAPPSHLIRVCGNS 232  
Db 144 QLVWDSPPPGTRRAVMAIKOSQHMTEVVRCPNHE--RCSDSDGLAPPOHLIRVCGNL 201  
QY 233 HAQVDEPITRGOSVLPVYPPPOVGTFTVLYNFMCNSSCGVGMNRRPILITVLETRD 292  
Db 202 RVEYLDNRNFRHSVYVYPPPEVGSCTTIHYNMCMSSCGMGNRRPILITLEDSS 261  
QY 293 GOVYLRRCFEARICACGRDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIK 352  
Db 262 GNLGRNSFEVRCACGGRDRTEENLRKKGEPRHHELPGSTRRALPNNT----SSSPQ 317  
QY 353 KRKSP-DDELLIYKRVKRETYEMLIKESLEL 384  
Db 318 PKRPLDGEYFTLIQIRGEREFEMRELNEALEL 350

RESULT 10  
US-08-390-516C-7  
Sequence 7, Application US/08390516C  
Patent No. 5708136  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,516C  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107,42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BBMB UT  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 393 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Harris, et al.,  
JOURNAL: Mol. Cell. Biol.  
VOLUME: 6  
ISSUE: 12  
PAGES: 4650-4656  
DATE: 1986

US-08-390-516C-7  
Query Match 30.18; Score 717.5; DB 1; Length 393;  
Best Local Similarity 41.24; Pred. No. 3,5e-60;  
Matches 156; Conservative 60; Mismatches 116; Indels 47; Gaps 9;

QY 11 LSPVFOHNDLEOPICSVQPIDLNFVDEPSEDGATNKIKESIMDCIRMDSDLSDMWP 70  
Db 14 LSOFTSDMLKLP-----NNVLSPLPSQAMDMLSDPDIEQWFT--DP--- 58  
QY 71 QYTLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSTFDALSP--SPA 126  
Db 59 -----GPDEAPRMEAPR--VAAP-ATPPAPADAPSPMLSSSV 97  
QY 127 PSNTDYGPHSPFVSPQOOSTAKSATWYTELKLYLQIAKTCPIQIKVMTPPGQAVI 186  
Db 98 PSQKTYGSGYFRLGFLHSGTAKSVCTCTSPALNKKMFCQIAKTCPVOLWDSPPPGTRV 157  
QY 187 RAMPYKKAHVTYVKKCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEPITRGOS 246  
Db 158 RAMATYKOSQHMTEVVRCPNHE--RCSDSDGLAPPOHLIRVCGNLVEYLDNRNFRHS 215  
QY 247 VLYPEPPOVGTFTVLYNFMCNSSCGVGMNRRPILITVLETRDGOVLRRCFEARIC 306  
Db 216 VVYPERPEVGSCTTIHYNMCMSSCGMGNRRPILITLEDSSGNLGRNSFEVRC 275  
QY 307 ACPGRDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKKRSP-DDELLIY 365  
Db 276 ACPGRDRTEENLRKKGEPRHHELPGSTRRALPNNT----SSSPQKKRPLDGEYFTLIQ 331  
QY 366 VRGRETYEMLIKESLEL 384  
Db 332 IGRGEREFEMRELNEALEL 350

RESULT 11  
US-08-431-357-2  
Sequence 2, Application US/08431357  
Patent No. 5721340  
GENERAL INFORMATION:  
APPLICANT: Halazonetis, Thanos D.  
TITLE OF INVENTION: p53 Proteins with Altered  
TITLE OF INVENTION: Tetramerization Domains  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr., PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/431,357  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/347,792  
FILING DATE: 28-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST58USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-5818  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 393 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-431-357-2

Query Match 30.1%; Score 717.5; DB 1; Length 393;  
 Best Local Similarity 39.7%; Pred. No. 3.5e-60;  
 Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

QY 11 LSPEVFOHIMFLEQ-----PICS-----VOPIDLN--FVDEPSEDGATNKIEISMDC 56  
 DB 14 LSGTFSDLMKLLPENNVLSPLPSQAMDMLSPDDIEQWTFDEDPDEA----- 63  
 QY 57 IRMODSLSDPMMPQYTNGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPVQPSST 116  
 DB 64 -----PRMPE-----AAP-----VAPAP-AAPIPA 83  
 QY 117 FDLALP-----SPAIPNTDYPGPHSPDVSVFOQSTAKSATWTSTELKLYCOIAKTCPI 172  
 DB 84 APAPAPSMPLSSVSPQKTYGSGYGRGLGHSHTAKSVCTCTSPALNKMFCQLAKTCPIV 143  
 QY 173 QIKYMPPOGAVIRAMPYVKAHEVTEVYKRCPNHLSREFNEGDIAPSHLIRVEGNS 232  
 DB 144 QLVWDSTPPPGTRVRAVMAIKQSOHMEVYRCPHNE--RCSDSGLAPPOHLIRVEGNL 201  
 QY 233 HAQVEDPITGRQSVLVPPEPVGTEFTTVLYNFMCSNCGVGMRRPILITVLETRD 292  
 DB 202 RVEYLDNRMTFRHSVYVPEPEVGSDCCTTHYNMCSNCGVGMRRPILITVLETRDSS 261  
 QY 293 GOVLGRCEARICACPGDRKADSDIRKQVSDSTKNGDGTGRPRFRONTNGIOMTSIK 352  
 DB 262 GNILGRNFEVYVACPGDRRTREENLRKGEHPHIELPGSTKRALPNNT-----SSSPQ 317  
 QY 353 KRSP--DDELLYLPVGRRETEMLKIKESLEL 384  
 DB 318 PKKKPLDGEYFTLQIRGRERFEMFRELNEALEL 350

## RESULT 12

US-08-390-515A-6  
 Sequence 6, Application US/08390515A  
 Patent No. 5756455

GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILEE  
 APPLICANT: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 STREET: 1001 G STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20001  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/390,515A  
 FILING DATE: 07-APR-1993  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107.42798  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100  
 TELEFAX: 202-508-9299  
 TELEX: 197430 BMB UT  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 393 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 PUBLICATON INFORMATION:  
 AUTHORS: Buchman, et al.,  
 JOURNAL: Gene  
 VOLUME: 70  
 PAGES: 245-252  
 DATE: 1988  
 US-08-390-515A-6

Query Match 30.1%; Score 717.5; DB 1; Length 393;  
 Best Local Similarity 39.7%; Pred. No. 3.5e-60;  
 Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

QY 11 LSPEVFOHIMFLEQ-----PICS-----VOPIDLN--FVDEPSEDGATNKIEISMDC 56  
 DB 14 LSGTFSDLMKLLPENNVLSPLPSQAMDMLSPDDIEQWTFDEDPDEA----- 63  
 QY 57 IRMODSLSDPMMPQYTNGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPVQPSST 116  
 DB 64 -----PRMPE-----AAP-----VAPAP-AAPIPA 83  
 QY 117 FDLALP-----SPAIPNTDYPGPHSPDVSVFOQSTAKSATWTSTELKLYCOIAKTCPI 172  
 DB 84 APAPAPSMPLSSVSPQKTYGSGYGRGLGHSHTAKSVCTCTSPALNKMFCQLAKTCPIV 143  
 QY 173 QIKYMPPOGAVIRAMPYVKAHEVTEVYKRCPNHLSREFNEGDIAPSHLIRVEGNS 232  
 DB 144 QLVWDSTPPPGTRVRAVMAIKQSOHMEVYRCPHNE--RCSDSGLAPPOHLIRVEGNL 201  
 QY 233 HAQVEDPITGRQSVLVPPEPVGTEFTTVLYNFMCSNCGVGMRRPILITVLETRD 292  
 DB 202 RVEYLDNRMTFRHSVYVPEPEVGSDCCTTHYNMCSNCGVGMRRPILITVLETRDSS 261  
 QY 293 GOVLGRCEARICACPGDRKADSDIRKQVSDSTKNGDGTGRPRFRONTNGIOMTSIK 352  
 DB 262 GNILGRNFEVYVACPGDRRTREENLRKGEHPHIELPGSTKRALPNNT-----SSSPQ 317  
 QY 353 KRSP--DDELLYLPVGRRETEMLKIKESLEL 384  
 DB 318 PKKKPLDGEYFTLQIRGRERFEMFRELNEALEL 350

## RESULT 13

US-08-390-515A-7  
 Sequence 7, Application US/08390515A  
 Patent No. 5756455

GENERAL INFORMATION:  
 APPLICANT: BURRELL, MARILEE  
 APPLICANT: HILL, DAVID E.  
 APPLICANT: KINZLER, KENNETH W.  
 APPLICANT: VOGELSTEIN, BERT  
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 STREET: 1001 G STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA



```

1 ZIP: 20001
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: PatentIn Release #1.0, Version #1.25
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/08/390,515A
16
17 FILING DATE: 07-APR-1993
18
19 CLASSIFICATION: 514
20
21 ATTORNEY/AGENT INFORMATION:
22
23 NAME: KAGAN, SARAH A.
24
25 REGISTRATION NUMBER: 32,141
26
27 REFERENCE/DOCKET NUMBER: 01107.42798
28
29 TELECOMMUNICATION INFORMATION:
30
31 TELEPHONE: 202-508-9100
32
33 TELEFAX: 202-508-9299
34
35 TELEX: 197430 BBWB UT
36
37 INFORMATION FOR SEQ ID NO: 7:
38
39 SEQUENCE CHARACTERISTICS:
40
41 LENGTH: 393 amino acids
42
43 TYPE: amino acid
44
45 TOPOLOGY: linear
46
47 MOLECULE TYPE: protein
48
49 HYPOTHETICAL: YES
50
51 ANTI-SENSE: NO
52
53 ORIGINAL SOURCE:
54
55 ORGANISM: Homo sapiens
56
57 PUBLICATION INFORMATION:
58
59 AUTHORS: Harris, et al.
60
61 JOURNAL: Mol. Cell. Biol.
62
63 VOLUME: 6
64
65 ISSUE: 12
66
67 PAGES: 4650-4656
68
69 DATE: 1986
70
71 US-08-390-515A-7

```

Db 318 PKKKPLDGEYFTLQIRGRERFEMFRELNEALEL 350

## RESULT 15

US-08-697-221-2  
; Sequence 2, Application US/08697221  
; Patent No. 5847083

## GENERAL INFORMATION:

APPLICANT: Halazonetis, Phanos D.  
TITLE OF INVENTION: Modified p53 Constructs and Uses  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr., PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/697,221  
FILING DATE:

## CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/004,802

FILING DATE: 22-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kodroff, Cathy A.

REGISTRATION NUMBER: 33,980

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 393 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-697-221-2

Query Match 30.1%; Score 717.5; DB 2; Length 393;  
Best local similarity 39.7%; Pred. No. 3.5e-60;

Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

QY 11 LSPEVFQHIWDFLEQ-----PICS-----VOPIDLN--FVDEPSFEDGATNKIEISMDC 56  
Db 14 LSQETFSDLMLKLLPENNVNLSPLPSQAMDDLMLSPDDIEQWTFEDPGPEA----- 63  
QY 57 IMQSDSLSDPMWPOYNTLGLNSMDOOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPST 116  
Db 64 -----PRMPE-----AAP-----VAPAP-AAPTPA 83  
QY 117 FDAISP-----SPAIPSNMTDYPGPHSFVSPFOQSSSTAKSATWTYSTEKKIKYCOIAKTCPI 172  
Db 84 APAPAPSPWLSVSSVSKTYGSGFRLGLHSGTAKSVTCTTSPALNKMFCOLAKTCPIV 143  
QY 173 QIKVMTPPPGAVIRAMPVYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNS 232  
Db 144 QLWVDSITPPETGRKRAVATIKOSQHMTEVVRCPNHE--RCSDSGLAPPHLIRVEGNL 201  
QY 233 HAQVEDPITGRQSVLVYEPPOVGEFTTVLYNFMCNSSCVGGMRRPILITVILETRD 292  
Db 202 RVEYLDNRNTFRHSVYVYEPPEVGSCTTIHNYMKNSSCMGMNRRPILITVILEDS 261  
QY 293 GQVIGRCFCFARICACPGRRKRADEDSIRKQOVSSTKNGDGTKRPFRONTHGIDWTSIK 352

Db 262 GNLLGRNSFEVRYCACPGDRDRKTEENLKKKGPHHELPPGSGTKRALPNNT-----SSSPQ 317  
QY 353 KRSP-DDELLYLPVGRRETYEMLTKIKESLEL 384  
Db 318 PKKKPLDGEYFTLQIRGRERFEMFRELNEALEL 350

Search completed: August 8, 2001, 01:36:44  
Job time: 4865 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 8, 2001, 00:20:14 : Search time 51.46 seconds  
(without alignments)  
663.160 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 2383

Sequence: 1 MSQSTQINEFLSPEVFOHIM.....PKSDVFFRHSKPPNRSYVP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	847.5	35.6	396	1 JH0631	cellular tumor ant
2	777.5	32.6	363	1 A29376	cellular tumor ant
3	764.5	32.1	367	1 S02193	cellular tumor ant
4	741.5	31.1	386	1 S51648	cellular tumor ant
5	732	30.7	391	1 S02192	cellular tumor ant
6	719.5	30.2	396	1 JH0633	cellular tumor ant
7	717.5	30.1	393	1 DNH053	cellular tumor ant
8	715	30.0	390	1 DNMS53	cellular tumor ant
9	714.5	30.0	393	1 S06594	cellular tumor ant
10	704	29.5	393	2 JC6176	tumor suppressor p
11	702	29.5	381	2 S38824	cellular tumor ant
12	699.5	29.4	391	2 JC6193	tumor suppressor p
13	259.5	10.9	77	2 T46226	cellular tumor ant
14	114.5	4.8	3942	2 T42730	Bassoon protein -
15	111.5	4.7	1819	2 T32008	hypothetical prote
16	110.5	4.6	2529	2 A56923	transcription fact
17	110	4.6	5762	2 A41819	proline-rich pepti
18	109	4.6	4273	2 C69679	polyketide synthas
19	108.5	4.6	701	1 S33709	DHR39-short protei
20	108	4.6	808	1 S33708	nuclear steroid/th
21	107	4.5	1681	1 D54689	protein-tyrosine-p
22	107	4.5	1894	2 C54689	protein-tyrosine-p
23	107	4.5	1912	2 A56178	protein-tyrosine-p
24	106.5	4.5	631	2 T31782	hypothetical prote
25	106.5	4.5	2578	2 A56922	transcription fact
26	105.5	4.4	395	2 A54949	synecan precursor
27	105	4.4	384	2 T49528	hypothetical prote
28	105	4.4	766	1 S61694	floculation suppr
29	105	4.4	909	2 T06635	hypothetical prote

30	104.5	4.4	1703	2 S15047	SNF2 protein - yea
31	104	4.4	1456	2 T01397	LTR gag/pol polypr
32	103	4.3	1533	2 T00344	hypothetical prote
33	102.5	4.3	780	2 A48143	HF-1 regulatory el
34	102.5	4.3	1203	2 T17415	mycelial surface a
35	102	4.3	628	2 S19150	hypothetical prote
36	100.5	4.2	1505	2 JC4851	hypoxia-inducible
37	100	4.2	600	2 T24447	hypothetical prote
38	99.5	4.2	526	2 T51372	hypothetical prote
39	99.5	4.2	1165	2 S27809	gtpase-activating
40	99.5	4.2	2359	2 T03094	A-kinase anchor pr
41	99.5	4.2	3938	2 T42761	Bassoon protein -
42	99	4.2	1621	2 T15264	hypothetical prote
43	99	4.2	1888	2 T14273	zinc finger protei
44	98.5	4.1	515	2 T40021	hypothetical prote
45	98	4.1	1213	2 A58198	serine/proline-ric

## ALIGNMENTS

```
RESULT 1
JH0631
cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-references: GB:M75145; NID:9213828; PIDN:AAA9605.1; PID:9213829
A:Experimental source: Liver
A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:164,167,227,231/Binding site: 21nc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (ser) (covalent) #status predicted

Query Match 35.6%; Score 847.5; DB 1; Length 396;
Best Local Similarity 45.4%; Pred. No. 6e-58;
Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;

QY 11 LSPVFQIHMDLEQPTCSVQPIDLNFVDEPSEDGATNKIEISMDCIKMODSDLSDPMP 70
      |||||:|
Db 12 LSGSFEDLW-----KNNLNLVAVQPPETE---SWV 39

QY 71 QYTLGLNLSMDQIIONGSSSTPYNTDHAQNSVTAPSPVQPS-STFDALS-PSPAIPS 128
      |||||:|
Db 40 GYDNF---MMEAPLQ-----VEPDPSLFEVSAATEPAPQPSITSLDNGSPPTSVPT 87

QY 129 NTDPVGPSPFVSFOOSTAKSATMTYSTEKLKLYCOIAKCPQIOWMPPPGAVIRA 188
      |||||:|
Db 88 TSDIPGALGFOLRLOSSTAKSVTCITSPDLNKLFCOLAKCPQIYVVDHPPGAVYRA 147

QY 189 MPVYKKAHEVTEVVKRPNMELISREFNQGQIAPPSHLIRVGNSHAQYVEDPITGRSVL 248
      |||||:|
Db 148 LAIKKLSADVADVVRRCRPHQSTSENNEGP-APRGHLVAVRGNGRSEYMEDGNTLRHSVL 206

QY 249 VPYEPVQVTEFTTVLYNFMQNSCVGAMNRPILITVLTETRDGQVUGRRCFARICAC 308
      |||||:|
Db 207 VPYEPVQVSECTTVLYNFMQNSCGMNRPIITITLETQEGQLLGRSFEVRCAC 266

QY 309 PGRKRKADSDSIRKQO--VSDFSKNGDGTGRKRPQO-NTHGIOVTSIKKRS---DDDE 360
      |||||:|
Db 267 PGRKRTEELINKQOETTLETTKTPRQGIKRAMKESLPAPOGASKKTSKSPAVSDDE 326

QY 361 LLYLPVGRGTEYEMLLIKESLELMQVLPQHTTETTYRQO 399
      |||||:|
```

Db 327 IYTLQIRGKREYEMLKRFNDSLESLVIVADAKYRK 365

# RESULT 2

A29376

cellular tumor antigen p53 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A29376; S61531; S72313; I51639

R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.

Oncogene 1, 71-78, 1987

A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein

A:Reference number: A29376; MUID:88143684

A:Accession: A29376

A:Molecule type: mRNA

A:Residues: 1-363 <SOU>

A:Cross-references: EMBL:X05191; NID:964961; PIDN:CAA28821.1; PID:964962

R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.

Oncogene 9, 109-120, 1994

A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus

A:Reference number: I51639; MUID:94134403

A:Accession: S61531

A:Molecule type: mRNA

A:Residues: 1-293,295-363 <HOE>

A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514

R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.

submitted to the EMBL Data Library, March 1994

A:Reference number: S72313

A:Accession: S72313

A:Molecule type: mRNA

A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOK>

A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514

C:Genetics: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho

F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match

Best Local Similarity 32.6%; Score 777.5; DB 1; Length 363;

Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

Db 2 SOSTQNEFLSEPVQHWIDLEPDI-----CSVQPIDNFVDEPSEDGATNKIEISMDCI 57

Db 4 SSETGMDPLSOETFEEDLSILPDPLQTVTCRLDLS- EFDYD-----LAADMT 52

Qy 58 RMQDSDLPMPMPQYTNGLNSMQOIQNGSSSTSPYNTDHAQNSVYAPSPYAPSPSTF 117

Db 53 VQGE-----GLMGN-----AVPTVT- 67

Qy 118 DALSPSPALPNTDYPGPHSPFVSFOOSSTAKSATWTYSTELKLYCOIAKTCGIQAKM 177

Db 68 -----SCAVPSTDYAGVYGLQDFQNGTAKSVTCYISPELAKLFCQLAKTCPLAVRVE 122

Qy 178 TPPOGAVIRAMPYKKAHEHTEVYKRCNPHLSREFNEGOIAPPSHLIRVEGNSHAQYV 237

Db 123 SPPPGSLIRKATAYKKSSEHVAEYVKKRCPHHERSEVPEGE--DAAPSHLMVEGNLQAYM 181

Qy 238 EDPTTGROSLVPEYPPQVGTETFTVLYNPMCNSSCVGGMNRRPILITVLETRDQVIG 297

Db 182 EDVNSGRHSVCVPEEGPQVTECTVLYNPMCNSSCVGGMNRRPILITVLETRDQVIG 297

Qy 298 RRCPEARICACPGDKRADEDS-IRKQVSDSTKNGDGTARRPQNTM--GIOMTSIKR 354

Db 242 RRCPEARICACPGDKRADEDS-IRKQVSDSTKNGDGTARRPQNTM--GIOMTSIKR 354

Qy 355 R---SPDELLVLPVRGRETYEMLKRESLELMQYLPHQTI 393

Db 293 LVVVDDEELFTLRKIRGRSRYEMIKRLNDLQESLSDQKV 334

# RESULT 3

S02193

cellular tumor antigen p53 - chicken

N:Alternate names: nuclear oncoprotein p53

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S02193

R:Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.

Nucleic Acids Res. 16, 11383, 1988

A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.

A:Reference number: S02193; MUID:89083584

A:Accession: S02193

A:Molecule type: mRNA

A:Residues: 1-367 <SOU>

A:Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F;161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match

Best Local Similarity 32.1%; Score 764.5; DB 1; Length 367;

Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

Qy 11 LSP-EVQHWIDLEPDIQSVQPIDNFVDEPSEDGATNKIEISMDCIRMQDSDLPMPM 69

Db 9 LEPTVEFMDLSMLPY---SMQOL-----PLEDSHMQNELS-----PLESDPPEPP 54

Qy 70 PLYNGLILNSMQOIQNGSSSTSPYNTDHAQNSVYAPSPYAPSPSTFALSPPAIPSN 129

Db 55 PPLPL-----AAAPPLMP--TPPRAAPSPVPEST 85

Qy 130 TDVPGPISFVVSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVTPPOGAVIRAM 189

Db 86 EDVGGGEFVGVGVGATKASVTCYSPVLYNPMCNSSCVGGMNRRPILITVLETRDQVIG 145

Qy 190 PVYKKAHEVTEYKRCNPHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPTGROSLV 249

Db 146 AVYKKEHVAEYVKKRCPHHERSGGTDG-LAPAQHLIRVEGNPQARYHDDETTKHSHVYV 204

Qy 250 PYPPQVGTETFTVLYNPMCNSSCVGGMNRRPILITVLETRDQVIGLRGCFEATACAP 309

Db 205 PYPPQVGTETFTVLYNPMCNSSCVGGMNRRPILITVLETRDQVIGLRGCFEATACAP 309

Qy 310 GRPKRADEDSIRKQVSDSTKNGD--TKRPPQNTMHIQMTSIIKKRSPDELLVLPVR 367

Db 265 GRPKRADEDSIRKQVSDSTKNGD--TKRPPQNTMHIQMTSIIKKRSPDELLVLPVR 367

Qy 368 GRETYEMLKRESLELMQ 386

Db 317 GRRREYEMLKRESLELMQ 335

RESULT 4

S51648

cellular tumor antigen p53 - bovine

N:Alternate names: tumor-suppressor protein p53

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S51648

R:dequiedt, F.; Williams, L.; Burny, A.; Kettmann, R.

submitted to the EMBL Data Library, September 1994

A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its

A:Reference number: S51648

A:Accession: S51648

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-386 <DEO>

A:Cross-references: EMBL:X81704; NID:9602332; PIDN:CAA57348.1; PID:9602333

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote

F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted



A:Cross-references: EMBL:X02469; EMBL:M60950; NID:935209; PIDN:CAA26306.1; PID:935210  
R:Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.  
Mol. Cell. Biol. 5, 1601-1610, 1985  
A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular  
A:Reference number: A55060; MUID:9526766  
A:Accession: A55060  
A:Molecule type: mRNA  
A:Residues: 1-71, 'P', '73-272, 'H', '274-393 <HAR>  
A:Cross-references: GB:R03199; NID:9189478; PIDN:AAA5989.1; PID:9189479  
R:Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Aral, N.; Rotter, V.  
Mol. Cell. Biol. 6, 4650-4656, 1986  
A:Title: Molecular basis for heterogeneity of the human p53 protein.  
A:Reference number: A93086; MUID:87089826  
A:Accession: A25397  
A:Molecule type: mRNA  
A:Residues: 1-78, 'T', '80-393 <HAR>  
A:Cross-references: EMBL:M14694; NID:9339813; PIDN:AAA61211.1; PID:9339814  
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line  
A:Accession: B25397  
A:Molecule type: mRNA  
A:Residues: 1-71, 'P', '73-78, 'T', '80-393 <HAR>  
A:Cross-references: EMBL:M14695; NID:9339815; PIDN:AAA61212.1; PID:9339816  
A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line  
R:Matlasiwski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.  
Mol. Cell. Biol. 7, 961-963, 1987  
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.  
A:Reference number: S42452; MUID:87144273  
A:Accession: S42452  
A:Molecule type: mRNA; DNA  
A:Residues: 66-71, 'P', '73-79 <MK12>  
A:Experimental source: clone lambda C113  
A:Note: 72-Cys was also found, and appears to represent a polymorphism  
A:Accession: S42453  
A:Molecule type: mRNA; DNA  
A:Residues: 66-79 <MK13>  
A:Experimental source: clone J6K  
R:Farrell, P.J.; Allen, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.  
EMBO J. 10, 2879-2887, 1991  
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.  
A:Reference number: I38082; MUID:92007731  
A:Accession: I38082  
A:Status: translated from GB/EMBL/DBJ  
A:Cross-references: EMBL:X60010; NID:9506432; PIDN:CAA42625.1; PID:9506443  
A:Note: deletion of a C nucleotide causes a frameshift at position 566  
A:Accession: I38083  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-189, 'LLSLISEKKELCWSIMWTFELFDIWNWCPMSRLALTF', 'VPSPTTTCVYPPANAA' <F01>  
A:Cross-references: EMBL:X60010; NID:9506432; PIDN:CAA42625.1; PID:9506443  
A:Note: deletion of a C nucleotide causes a frameshift at position 566  
A:Accession: I38083  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-192, 'R', '194-393 <F02>  
A:Cross-references: EMBL:X60011; NID:9506434; PIDN:CAA42626.1; PID:9506435  
A:Accession: I38084  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-245, 'T', '247-393 <F04>  
A:Cross-references: EMBL:X60013; NID:9506438; PIDN:CAA42628.1; PID:9506439  
A:Accession: I38086  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236, 'I', '238-393 <F05>  
A:Cross-references: EMBL:X60014; NID:9506440; PIDN:CAA42629.1; PID:9506441  
A:Accession: I38087  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-247, 'Q', '249-393 <F06>  
A:Cross-references: EMBL:X60015; NID:9506442; PIDN:CAA42630.1; PID:9506443  
A:Accession: I38088



A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>  
A:Cross-references: EMBL:X60016; NID:9506444; PIDN:CAA42631.1; PID:9506445  
A:Accession: 138089  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-247, 'O', 249-393 <F08>  
A:Cross-references: EMBL:X60017; NID:9506446; PIDN:CAA42632.1; PID:9506447  
A:Accession: 138090  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>  
A:Cross-references: EMBL:X60018; NID:9506448; PIDN:CAA42633.1; PID:9506449  
A:Accession: 138091  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-212, 'O', 214-393 <F10>  
A:Cross-references: EMBL:X60019; NID:9506450; PIDN:CAA42634.1; PID:9506451  
A:Accession: 138092  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-253, 'D', 255-393 <F11>  
A:Cross-references: EMBL:X60020; NID:9506452; PIDN:CAA42635.1; PID:9506453  
A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991  
R:Futurel, P.A.; Barrett, J.C.; Wiseman, R.W.  
Nucleic Acids Res. 19, 6977, 1991  
A:Title: An Alu polymorphism intragenic to the TP53 gene.  
A:Reference number: 138093; MUID:92107726  
A:Accession: 138093  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-393 <FUT>  
A:Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214  
R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirata, S.; Nakatani, T.  
Cancer Res. 51, 5800-5805, 1991  
A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line  
A:Reference number: A44905; MUID:92034678  
A:Accession: A44905  
A:Molecule type: DNA  
A:Residues: 246-247, 'W', 249-250 <YAM>  
A:Cross-references: GB:S63157; NID:9237829; PIDN:AAB20140.1; PID:9237830  
A:Note: sequence extracted from NCBI backbone (NCBI:63157, NCBI:63158)  
R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.  
Oncogene 6, 1067-1071, 1991  
A:Title: Use of the single strand conformation polymorphism technique and PCR to detect  
A:Reference number: 158354; MUID:91296386  
A:Accession: 158354  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 244-247, 'W', 249-252 <HEN1>  
A:Cross-references: GB:S41969; NID:91679931; PIDN:AAB19324.1; PID:9232814  
A:Accession: 178850  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 274-277, 'S', 279-282 <HEN2>  
A:Cross-references: GB:S41977; NID:91679932; PIDN:AAB19325.1; PID:9232816  
R:Chow, V.T.; Quek, H.H.; Jock, E.P.C.  
Cancer Lett. 73, 141-148, 1993  
A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblastoid cell line  
A:Reference number: 152681; MUID:94036762  
A:Accession: 152681  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 327-331, 'DQTSFQKENC' <CHO>  
A:Cross-references: GB:S66666; NID:9436292; PIDN:AAB28601.1; PID:9436293  
A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-Lymphoblastoid cell line  
R:Peterson, G.; Song, D.; Hiegle-Deert, B.; Oldenburg, I.; Bautz, E.K.F.  
Mol. Gen. Genet. 249, 425-431, 1995  
A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragments  
A:Reference number: S60151; MUID:96133682  
A:Accession: S60153

A:Molecule type: DNA  
A:Residues: 3-44 <PEP>  
R:Yang, C.V.; Lee, W.M.F.  
J. Biol. Chem. 264, 18019-18023, 1989  
A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP  
Query Match 30.1%; Score 717.5; DB 1; Length 392;  
Best Local Similarity 41.2%; Pred. No. 6.7e-48;  
Matches 156; Conservative 60; Mismatches 116; Indels 47; Gaps 9;  
11 LSPEVFOHIMDFLEQPIGVQPIDLNFVDEPSEDEGATKRIEISMDICIMODSDLSPPMP 70  
14 LSQEFSSDLWKLP-----NNVLSPLPSQAMODMLSPDDIQWTE--D--- 58  
71 QYTNGLNLSMDQIQNSSSTSPYNTHAQNSVTAPEPYAPSPSTFALSP---SPAI 126  
59 -----GPDAPMPPEAAR--VAAPV-AAPTPAAPAPASWPLSSV 97  
127 PSNTDYPGPHSPFVSFOOSSTAKSATWTSTELKLYCOIKTCPIQIKVTPPGAGAVI 186  
98 PSQKTYQSGYGFRLGFLHSGTAKSVCTTSPALNMFQOLAKTCVQLWMDSTPPGTRV 157  
187 RAMPYKRAEHVTEVVKRCPNHELSEFNEGOIADPSHLIRVGNSHAQYEDPTTGRS 246  
158 RMAIYKQSQHWTEVVRRCPHHE--RCSDSQDLAPQHLIRVEGNLRYEYLDLDRMTFRHS 215  
247 VLVPYEPQVGFETFTVLYNEMCNSSCYGMMRRPILIVLETGQVLRGRCEAHC 306  
216 VVVPYEPQVSDCTTHYNYMNCSSCMGMMRRPILITILESSGNLRNSEEVC 275  
307 ACPGRKRADEDSIRKQVOSTKNGDGTKRFQNTQIGWTSIKRRSP--DDELLVLP 365  
276 ACPGRKRTTEENLKKKEPHELPPGSTKRALPNNT-----SSFPQKKKPLDGEYFTLG 331  
366 VGRTEYEMLKIKESLEL 384  
332 IGRGRFEMFRELNEALEL 350  
RESULT 8  
DNM53  
cellular tumor antigen p53 - mouse  
N:Alternate names: oncoprotein p53  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Aug-1985 #sequence\_revision 04-Oct-1996 #text\_change 11-May-2000  
C:Accession: A22739; S06336; A02684; S38823; S40014; I48703  
R:Blenz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.  
EMBO J. 3, 2179-2183, 1984  
A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.  
A:Reference number: A22739; MUID:85027173  
A:Accession: A22739  
A:Molecule type: DNA  
A:Residues: 1-134, 'V', 136-390 <BIE>  
A:Cross-references: GB:X00876; NID:9871420; PIDN:CAA25420.1; PID:9871421; GB:X01237;  
R:Chumakov, P.M.  
Bioorg. Khim. 13, 1691-1694, 1987  
A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.  
A:Reference number: S06336; MUID:88221682  
A:Accession: S06336  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-134, 'V', 136-390 <CHU>  
R:Zakut-Houri, R.; Oren, M.; Blenz, B.; Lavie, V.; Hazum, S.; Givol, D.  
Nature 306, 594-597, 1983  
A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.  
A:Reference number: A02684; MUID:84068204  
A:Accession: A02684  
A:Molecule type: mRNA  
A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'T', 235-390 <ZAK>  
A:Cross-references: GB:X01237; GB:X01700; NID:953575  
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
Mol. Cell. Biol. 6, 3232-3239, 1986  
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A: Molecule type: mRNA  
A: Molecule type: mRNA  
A: Residues: 1-167, 'G', 169-390 <RA3>  
A: Cross-references: EMBL:M13873; NID: g200200; PID: AAS439682.1; PID: g200201  
A: Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.  
Nucleic Acids Res. 12, 5609-5626, 1984  
A: Title: Cloning and expression analysis of full length mouse cDNA sequences encoding tyrosine phosphatase  
A: Reference number: 148703; MUID: 84272240  
A: Accession: 148703  
A: Status: translated from GB/EMBL/DBJ  
A: Molecule type: mRNA  
A: Molecule type: mRNA

A: cross-references: 1-411, R: 49-78, 'OM', 82-390 <RES>  
C: comment: This DNA-binding protein plays an essential role in the regulation of cell division. The tetramer association region may exhibit a beta-turn, beta-sheet, beta-turn.  
C: keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;  
F: 16-46/Domain: transcription activation #status predicted <TRPA>  
F: 99-289/Region: conserved region I  
F: 108-121/Region: L1 loop  
F: 114-139/Region: conserved region II  
F: 160-192/Region: L2 loop  
F: 168-178/Region: conserved region III  
F: 231-252/Region: conserved region IV  
F: 233-248/Region: L3 loop  
F: 267-283/Region: conserved region V  
F: 313-319/Region: nuclear location signal  
F: 319-357/Region: tetramer association  
F: 77-9, 12, 18, 23, 37/Binding site: phosphate (Ser) (covalent) #status predicted  
F: 113, 176, 235, 239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F: 312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted  
F: 389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

```

Query Match          30.0%; Score 715; DB 1; Length 390;
Best Local Similarity 38.3%; Pred. No. 1e-47;
Matches 166; Conservative 62; Mismatches 125; Indels 80; Gaps 13

QY      2 SOSTQTNEF--LSPEVFQHIWDFLEQPLGCSQPIDLNFVDEPSSDGAATNKIEISMDCIHQ 60
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      7 SOSDLSLELPLSQETFSGLKKLL-----PPED-----ILSPHC----- 40

QY      61 DSDLSPPMNPQYTNLGLNLSMDQQLQNGSSSTSPYNTDHAQNSVT--APSPYQPSSTPDA 119
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      41 -----MDLLLPQ-----DVEEFEGPSEALRVSGAPRAQDPYIETGPVA----- 81

QY      120 LSPSPA-----IPSNTDYRGPSPSFDVSFOQSSSTAASATWTSYTELKLKYQIATKCP 171
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      82 --PAPATPWLSSFPVSQKTYGNGTGFHGLGFSQSTASVMCTYSPLINKLFQCLAKTCP 139

QY      172 IQIKWTPPGGAVYTRAMPVYKKAHEVEYVKRCNHHSLSREFNEGQ--IAPSHLIRVEG 230
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      140 VOLWVSATPPAGSRVRAAIYKKSQHMFEVVRCPCHNE--RCSDGGLAPQHLIRVEG 196

QY      231 NSHAQVEDPPLTGRSLVLYPEPPOVGEFTPTVLYNFCMNSCCVGNRRRPIILTYVLET 290
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      197 NLPEYLEDROTFRHSVVAYPEPEAGSEYTTIHYKYMCSNGCMGNRRRPIILTYLED 256

QY      291 RDGOVLCGRCEAFARICACPRGDRRADEPSIRKQOVSSTKNGDTKKPFRONTHGIGMTS 350
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

Db 257 SSGNLLRGSEFEYRWCACBGRDRTTEENFRKKKFLVCELPRLPGSAKRALPYCT---SASP 313  
QY 351 IKRRSPFDDELLLYPVGRGHEVYEMLKIKESLEIMOVLPDHTTE-----TYR 397  
Db 314 PQRKRPDLGSEYFTLLRIGRRKRFEMRELNEALTKD---AHATSESGDSRAHSSYLTKK  
QY 398 QQQQQQDQHLLQK 410  
Db 371 GQSTSRHKKTKYWK 383

RESULT 9  
S06594

cellular tumor antigen p53 - green monkey  
C:Species: Cercopithecus aethiops (green monkey, grivet)  
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C.Accession: S06594  
R:Rigaudy, P.; Eckhardt, W.  
Nucleic Acids Res. 17, 8375, 1989  
A>Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p5  
A.Reference number: S06594; M01D:90045967  
A.Accession: S06594  
A.Molecule type: mRNA  
A.Residues: 1-993 <RIG>  
A.Cross-references: EMBL:X16384; NID:922795; PIDN:CAN34420.1; PID:922796  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: Apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho  
E:116,119,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

	Query Match	30.0%;	Score 714.5;	DB 1;	Length 393;
	Best Local Similarity	41.2%;	Ped. No. 1.1e-47;		
	Matches 156;	Conservative	63;	Mismatches 113;	Indels 47; Gaps
Qy	11 LSPVFOHIDFLEOPICISYQPIDLPFDEPESDGAINKIEISMDCIRMODSLSPMPWP	70			
Dd	14 LSQETSEDMKLILPE-----NNLSPLPQAADDMLDSP-----DLA--QW-	53			
Qy	71 QYNLGLIAMSQQQLONGSSSTSPINDHAONSYTAPSAPOGSSFTFDALSP----	SPI	126		
Dd	54 -----LTEDGGDPPEAPRMSEAAPH--MAPTP--AAPTPAAPAPASWPLSSSV	97			
Qy	127 PSLNTDYPGHSDVSFFQOOSTAKSATMTMYSPFLIKLYCOATKACGCCTGTCTTTTC				

```

Db      98  PSOKTYHSGSYFRLGFLHSGTASVTCYISPLDNKMFQGLAKTQVPLWMDSTPPGSGRY 15
.Qy     187  RAMPYRKAEHVEVYVRCGNHLSLSEFNESGDIAPPSHLRVEGNSHAQYVENDPIRGROS 24
Db      158  RMAIYIKOSQMTYVYARCNHE--RCSQSDLAAPQHLRVEGNLIRVEYSDDRNTPFRS 21
.Qy     247  VLYVPEPQVGETFTVLYVFNKSNSSCVGNNRRPILITLYLERGQVLYGRCEARIC 30
Db      216  VVVPPEPEPGESDCTIHYNYKMSNCMGMMRRPILITLITLEDSSNLLGRNSEFVRQ 27
.Qy     307  ACPGRDAKDEDSIRKQVSDSTKNGDCTKRPRPQONHGIQMTSIKRRSP--DELLLYP 36
Db      276  ACPGRDRRTDEENFRKKKGPCHELRPGSTKALPNNT---SSSDPPKKKPLDGEYFTIQ 33
.Qy     366  VGRGTEYEMLKIKESLEL 364
Db      332  IGRGREREMERLEALEL 350

```

RESULT 10  
JC6176  
tumor suppressor protein p53 - Chinese hamster  
C:Species: Cricetus griseus (Chinese hamster)  
C:Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 23-Jul-1999  
C:Accession: JC6176  
R:Lee, H.; Larner, J.M.; Hamlin, J.L.  
Gene 184, 177-183, 1997  
A:Title: Cloning and characterization of Chinese hamster p53 cDNA.

A:Reference number: JC6176; MUID:97183659  
 A:Contents: liver  
 A:Accession: JC6176  
 A:Molecule type: mRNA  
 A:Residues: 1-393 <LEF>  
 A:Cross-references: GB:50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230  
 C:Comment: This protein is a multimer. It plays the central role in a complex DNA damage  
 lition, and recombination by protein/protein interactions.  
 C:Genetics:  
 A:Gene: p53  
 C:Superfamily: cellular tumor antigen p53  
 C:Keywords: liver; tumor

Query Match 29.5%; Score 704; DB 2; Length 393;  
 Best Local Similarity 38.6%; Pred. No. 7.4e-47;  
 Matches 165; Conservative 66; Mismatches 134; Indels 60; Gaps 11;

QY 11 LSPVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDICRMODSDLSDPW-- 68  
 DB 14 LSGTEFSDLMKLT-----PNNVLTSLPSSDS-----IEELFISENVTG 52

QY 69 WPOITNGLNSMDQOIONGSSSTPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIP 127  
 DB 53 WLEDSGGAL-----QGVAAAAAST-----AEDPVETEPAPVASAPATPWLSSS--VP 98

QY 128 SMDYGPSPVDFVFSQOSTAKSATWTSTELKLYCOIATCPDIOTKVMPPPGANVIR 187  
 DB 99 SYKTFQGDYGFRLGLFSLGTAQSVCTYSPSLNFCOLATCPVQALVWVNSTPPGTRVR 158

QY 188 AMPYKAEHTEVYKRCRNHELSEFNEGOIAPPSHLIRVGNSSHAQYVDPTGROS 247  
 DB 159 AMAIKKIQYVTEVYRCRPHNERSSEGD--SLAPQHLIRVGNLHAEYLDKQTFRHSV 216

QY 248 LVPEPPQVGEFTVLYXNFNCSSCYGAMRRPILITVLETGQVGLGRCEARICA 307  
 DB 217 VVPEPEVSGDCTTHNMYNCSGCMNRRLITLITLEDSSGMLGNSEFVRICA 276

QY 308 CPGRDRADEDSIRKQVSDSTKNGDGTKRPRFONTHGIQMTSIKKRSPDELLYLPR 367  
 DB 277 CPGRDRTEENKPFQKGPCELPKSAKRALPTNT---SSPPPKKTTLDGEYFTLKIR 333

QY 368 GRETEMLIKIKESLELMQYLPQHTIE---TYRQOQOQHQLLOKHLISACFRNEL 421  
 DB 334 GHEFFKMFQELNEALELKDQAQSGSEDNCAHSSYLSKKGQASRLKLTMI----- 385

QY 422 VERRRPT 429  
 DB 386 ---KREGP 390

RESULT 11  
 S38824  
 cellular tumor antigen p53, minor splice form - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
 C:Accession: S38824; S35478  
 R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Kotter, V.  
 Mol. Cell. Biol. 6, 3232-3239, 1986  
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.  
 A:Reference number: S38822; MUID:87064640  
 A:Accession: S38824  
 A:Molecule type: mRNA  
 A:Residues: 1-381 <ARA>  
 A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203  
 R:Han, K.A.; Kulesz-Martin, M.F.  
 Nucleic Acids Res. 20, 1979-1981, 1992  
 A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different tiss  
 A:Reference number: S35478; MUID:92253421  
 A:Accession: S35478  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-381 <HAN>

A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203  
 A:Note: the nucleotide sequence was submitted to the EMBL data library, July 1988  
 C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks  
 s not known.  
 C:Superfamily: cellular tumor antigen p53  
 C:Keywords: alternative splicing; phosphoprotein; zinc  
 F:1-44/Domain: transcription activation #status predicted <TRA>  
 F:16-26/Region: conserved region I  
 F:99-289/Domain: DNA-binding core #status predicted <BC>  
 F:108-121/Region: L1 loop  
 F:114-139/Region: conserved region II  
 F:160-192/Region: L2 loop  
 F:168-178/Region: conserved region III  
 F:231-252/Region: conserved region IV  
 F:233-248/Region: L3 loop  
 F:267-283/Region: conserved region V  
 F:313-319/Region: nuclear location signal  
 F:319-357/Region: tetramer association  
 F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted  
 F:173,176,235,239/Binding site: zinc (Cys, His, Cys) #status predicted  
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

Query Match 29.5%; Score 702; DB 2; Length 381;  
 Best Local Similarity 40.4%; Pred. No. 1e-46;  
 Matches 159; Conservative 58; Mismatches 113; Indels 64; Gaps 11;

QY 2 SOSTQTNEL-LSPEVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDICRMQ 60  
 DB 7 SQSDISLELPQSTEFSGIMKLT-----PPED-----LPSPHC----- 40

QY 61 DSDSDPMPMPQYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVT-APSPYAQPSSTFDA 119  
 DB 41 ---MDLLLPQ-----DVEEFPEGSEALRVSGAPADPTEPGRVA----- 81

QY 120 LSPSPA-----IPSNTDYGPSPVDFVFSQOSTAKSATWTSTELKLYCOIATCP 171  
 DB 82 --PAPATPWLSSVFPSTQYQGVNGFHLGLQSGTAKSVCTYSPSLNFCOLATCP 139

QY 172 IQIKVMPPPPGANVIRAMPYKAEHTEVYKRCRNHELSEFNEGO-IAPPSHLIRVGN 230  
 DB 140 VQLVASATPAGSRVAATYKKSQHMTEVYRCRPHNE---RCSGDGLAPQHLIRVGN 196

QY 231 NSHAQYVEDPTGROSQVLYPEPVQVGEFTVLYXNFNCSSCYGAMRRPILITVLET 290  
 DB 197 NLYPEILEDRTGTPRHSVYVPEPEPAGSEYTHYKYNCSGCMNRRLITLITLED 256

QY 291 RDGQVGLGRCEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPRFONTHGIQMTS 350  
 DB 257 SSGNGLGRDSEFVAVCAACPGDRRTTEENFRKKVLCPELPKSAKRALPTCT---SASP 313

QY 351 IKRRSPDELLYLPVGRETEMLIKIKESLEL 384  
 DB 314 POKKKPLDGEYFTLKIRKRFEMFRELNEALEL 347

RESULT 12  
 JC6193  
 tumor suppressor p53 - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000  
 C:Accession: JC6193  
 R:Le Gass, F.; May, P.; Ronco, P.; de Fromental, C.C.  
 Gene 185, 169-173, 1997  
 A:Title: cDNA cloning and immunological characterization of rabbit p53.  
 A:Reference number: JC6193; MUID:97208869  
 A:Accession: JC6193  
 A:Molecule type: mRNA  
 A:Residues: 1-391 <LEA>  
 A:Cross-references: EMBL:X90592; NID:g1532043; PIDN:CAA62216.1; PID:g1532044  
 C:Genetics:  
 A:Gene: p53  
 C:Superfamily: cellular tumor antigen p53

C:Keywords: tumor

Query Match  
 Best Local Similarity 29.4%; Score 699.5; DB 2; Length 391;  
 Matches 156; Conservative 56; Mismatches 102; Indels 81; Gaps 10;

QY 11 LSPVFOHIDFL-EOPICSVQ---PID-----LNVDPSEEGATNKIEISMDICR 58  
 DB 14 LSOETFDLWKLIPENNLLTTSINPVDLLSEADVANLNLNDPEG----- 60  
 QY 59 MODSDSDPMPOQYTNGLNLSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAPSSNFD 118  
 DB 61 -----LRVP-----APAEBA-PAPAP 77  
 QY 119 AL-SPSPA-----IPNTDYPGPHSPDVSFOQSSSTAKSTWTYSLEKLKCOIAKT 169  
 DB 78 ALAAPAPATSWPLSSVSPQKTYHGNNGFRGLGFLHSGTAKSVTCTYSPCLNKLFCQIAKT 137  
 QY 170 CPLOIVMTPPGAVIRAMPYKAEVTEVYKRCNPHELSREFNEGOIAPSHLIRVE 229  
 DB 138 CPVQLMVDSTPPGTRVRAMALYKKSQHMTEVYRCPHHE--RCSDDGLAPPOHLIRVE 195  
 QY 230 GNSHAQVEDPTTGROSVLVPEPPOVGTETTYLYNPMCNSSCGVMNRPLIITVLE 289  
 DB 196 GMLRAEYLDNRTERHVSIVVPEPEVSGDCTTHYNTMCSGCMGMRPLIITVLE 255  
 QY 290 TNDGVLGRCEARICRGROKADDSIRKQVSDSTKNGDTKRPRTGHIQMT 349  
 DB 256 DSSGLLRNRFSEVAVACACPRDRTEENFRKGEPCPELPSSSKRALPTT--TDS 313  
 QY 350 SIKRRSRDDELVLVPAVGRETYEMLIKESLEL 384  
 DB 314 POTKKKPLDGEYFLIKIRGEREFEMRELNEALEL 348

RESULT 13  
 146226  
 cellular tumor antigen p53 - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 05-May-2000  
 R:Accession: I46226  
 R:Deviljee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.  
 Anticancer Res. 14, 2039-2046, 1994  
 A>Title: The canine p53 gene is subject to somatic mutations in thyroid carcinoma.  
 A:Reference number: I46226; MUID:95150524  
 A:Accession: I46226  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-77 <DEV>  
 A:Cross-References: GB:I27630; NID:9508454; PIDN:AAC37327.1; PID:9508455  
 A:Gene: p53  
 C:Genetics:  
 C:Superfamily: cellular tumor antigen p53

Query Match  
 Best Local Similarity 10.9%; Score 259.5; DB 2; Length 77;  
 Matches 47; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 194 KAEHTEVYKRCNPHELSREFNEGOIAPSHLIRVEGNSHAQVEDPTTGROSVLVPEP 253  
 DB 1 KSEFVTEVYRCPHHEKCSDDSG-LAPPOHLIRVEGNLAKAYLDRTYFRHSVVPYEP 59  
 QY 254 PÖVGTEFTYLYNPMCN 271  
 DB 60 PEVGEFTYTHYNYMNS 77

RESULT 14  
 T42730  
 Bassoon protein - mouse

C:Species: Mus musculus (house mouse)  
 C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T42730  
 R:Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; W  
 J. Cell Biol. 142, 499-509, 1998  
 A>Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively local  
 A:Reference number: 222249; MUID:98345363  
 A:Accession: T42730  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3942 <DIE>  
 A:Cross-References: EMBL:Y17034; NID:93413809; PIDN:CAA76598.1; PID:93413810  
 A:Experimental source: Strain 129 SVJ  
 A:Genetics:  
 A:Map position: 9P1  
 A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1  
 A>Note: Bassoon  
 C:Function:  
 A:Description: may be involved in cytomatrix organization at the site of neurotransmi  
 A>Note: component of the presynaptic cytoskeleton  
 C:Keywords: coiled coil; zinc finger

Query Match  
 Best Local Similarity 4.8%; Score 114.5; DB 2; Length 3942;  
 Matches 113; Conservative 61; Mismatches 190; Indels 169; Gaps 25;

QY 1 MSOSTQTFNEFSPVPHIDFLFOPI-----CSVOPIDLNVDPSEB----- 44  
 DB 2038 LGGLOYGSTFD---LRHPDLISHPLPLRRYSVSNITSDHRYGPRDVGFOGASIAQ 2094  
 QY 45 -GATNKEISMDICRMQDSDLPMPPOQYTNGLNLSMDQO-IONGSSSTSP-----YNTD 98  
 DB 2095 YSATAREISRM-----AALNSMDQIGKHSGGSGGLDVOYOPQ 2135  
 QY 99 HAQNSVTAPSPYAPSS-----TFDALSPPAITSNTDYPGPHSPDVSFOQSSSTAKSAT 152  
 DB 2136 HGP-GLSARQGLAPLRSGILGNPTPEGOPS---PGNLAQCPAASQATAVRQLPSTAT 2191  
 QY 153 -----WYSTELKLYCOIAKTCPIQIR---VMTPPGAVIRAMPYKAEVTEVYK 203  
 DB 2192 VRAADGMIST---INPIAATLPTTQPASVLRPMVRGMIR-----PYVSGGYT 2239  
 QY 204 RCPNHELSREFNEGOIAP-----PSHLIRVEGNSHAQVEDPTTGROSVLVPE-PPQV 257  
 DB 2240 AVPLSLTR---VPMIARVPLGPRGLYRPAPRP-----PIA---SSVPAEGVYLG 2287  
 QY 258 TETFTVLYNPMCNSSCGVMNRPLIITVLETRDGOVLGRCEARICACRG----- 310  
 DB 2288 KPAAT-----KASGAGGPRPELPAGVARREPFSTTAPAVIKAPVAPAPAPAPP 2340  
 QY 311 -----RDKAEDDSIRKQVSDSTKNGDTKRPRTGHIQ 347  
 DB 2341 GOKPAGEAAGSGSVLSRPASEKEASQEDRQKOE-----Q 2379  
 QY 348 MTSIKRRSRDDELILYV-----RCRETYEMLIKESLELMOYLPOHTIET 395  
 DB 2380 LIQERREVELEKRIQRLQDELREVRVELQHRHREBQL--VQNELQLOITIKOHLQ- 2436  
 QY 396 YRQOQOQHLLQKHLISACFNELEVPERREPKQSDVFFHNSAPPNRSYVP 448  
 DB 2437 -QOOEEROAQFALQREQLAQ--QRQLEQIQOQLOQLOLEQOKOROKAPPP 2486

RESULT 15  
 T32008  
 hypothetical protein K106.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T32008  
 R:Davidson, S.; Wohlmann, P.; Mullen, G.  
 submitted to the EMBL Data Library, July 1997  
 A:Description: The sequence of C. elegans cosmid K106.

A:Reference number: 221111  
A:Accession: T32008  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1819 <NAV>  
A:Cross-references: EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESP:K10G6.3  
A:Experimental source: strain Bristol N2; clone K10G6  
C:Genetics:  
A:Gene: CESP:K10G6.3  
A:Map position: 2  
A:Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3

Query Match 4.7% Score 111.5; DB 2; Length 1819;  
Best Local Similarity 19.4% Pred. No. 4.2;  
Matches 76; Conservative 65; Mismatches 153; Indels 97; Gaps 15;

```
QY 84 QIONGSSSTPYNTDHAONS--VTAP-SPYAQPSSTFDALSPSPAIPSNMDYPGPHSFDV 140
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 749 KVAASSSSNSASRRPSPQSTPATAPATAPMLQASQAPQLQAPPSPMET-----TATV 802
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 141 SFOOSSTAKSTWTYSTELKLYCOIAKTCPIQIKVMTPPQGAVIRAMPVYKKAENVTE 200
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 803 TYRTTYPPSVANTWTEKAQLISPKPRSQIFSEASSMTVGDLRAQCHQOKMDQIQ 862
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 201 V-----VKRCPNHELSEFNEGQIAPPSHLI-----RVEGNSHAQYVEDPITGROS 246
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 863 IQFOQOQOQRRQNHQOQOQAGRIPPRRPNPILNOYONPQOYONHONOMLNP1--RQP 920
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 247 VL--VPEPPOVGETFTTVLVNFMCSNCGVMNRRLIIVT---LETROGVLGRRRC 300
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 921 LLAGPPPPPKKGLI-----EHNKNTDLVLTSEPLAERMDAK---RRS 960
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 301 FEARICA-----CPGRDKADEDSIRKQVSDSTKNGDGTKRPFRONTHG 345
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 961 SEGVAVTSTPLRP1QLPQRSQAPAPSRKQOQOQPPVAYOVQNGRPLRPMLPQLNPHN 1020
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 346 IQMTSIKKRRSPDELLYLVPYRGREYEMLKIKESLELMOYLPOHTIETVROO--QOQ 403
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1021 QO-----QOHOMLHQSOMNTQOYQOYQO--VQHVQOQOQNLQNO 1056
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 404 HQHLLQKHLLSACFRNELVEPRRETPOKSDV 434
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1057 HNHQOQHNO-----QNOQOQAPGNRSRSHSNV 1082
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

Search completed: August 8, 2001, 01:37:49  
Job time: 4655 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 8, 2001, 01:35:41 : Search time 51.14 Seconds  
(without alignments)  
300.087 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 2383  
Sequence: 1 MSQSTQTNFELSPVEFGHIM.....PKSDVFRHSPKPNRSVYP 448

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1297.5	54.4	636	1 P73_HUMAN	O15350 homo sapien
2	1296.5	54.4	637	1 P73_CERAE	O9SK8K cercoptithc
3	847.5	35.6	396	1 P53_ONCMY	P25035 oncorhynch
4	819.5	34.4	369	1 P53_BARBU	O9W678 barbush barb
5	805.5	33.8	373	1 P53_BRARE	P79734 brachydantio
6	800	33.6	376	1 P53_ICTPD	O83379 ictalurus p
7	777.5	32.6	363	1 P53_XENLA	P07193 xenopus lae
8	776	32.6	367	1 P53_TETMU	O9W679 tetraodon m
9	770	32.3	386	1 P53_FELCA	P41685 felis silve
10	767	32.2	386	1 P53_PIG	O9TUB4 sus scrofa
11	764.5	32.1	367	1 P53_CHICK	P10360 gallus galli
12	753.5	31.6	381	1 P53_CANFA	O29537 canis famli
13	746	31.3	351	1 P53_ORVLA	P79820 oryzias lat
14	741.5	31.1	386	1 P53_BOVIN	O29628 bos taurus
15	736	30.9	391	1 P53_MARMO	O36006 marmota mon
16	732	30.7	391	1 P53_RAT	P10361 rattus norv
17	730.5	30.7	391	1 P53_CAVPO	O2WUT6 cavia porce
18	729.5	30.6	393	1 P53_TUPGB	O3TAL4 tupata glis
19	727.5	30.5	382	1 P53_SHEEP	P51664 ovis aries
20	719.5	30.2	396	1 P53_MESAU	O00366 mesocricetu
21	718	30.1	366	1 P53_PLAFE	O12946 platichthys
22	717.5	30.1	393	1 P53_HUMAN	P04637 homo sapien
23	715.5	30.0	393	1 P53_MACRA	P56442 macaca fasc
24	715	30.0	390	1 P53_MOUSE	P02340 mus musculu
25	714.5	30.0	393	1 P53_CERAE	P13481 cercoptithc
26	713.5	29.9	393	1 P53_MACMU	P56424 macaca mula
27	710.5	29.8	342	1 P53_XIPHE	O57538 xiphophorus
28	709.5	29.8	342	1 P53_XIPMA	O92143 xiphophorus
29	708	29.7	393	1 P53_CRIGR	O09185 cricetus
30	699.5	29.4	391	1 P53_RABIT	O93530 oryctolagus
31	696	29.2	314	1 P53_SPEBB	O64662 spermophilu
32	689.5	28.9	280	1 P53_HORSE	P79892 equus caball
33	591.5	24.8	207	1 P53_EQUAS	O29480 equus asinu

# ALIGNMENTS

RESULT 1	P73_HUMAN	STANDARD:	PRT: 636 AA.
AC	O15350:O15351; Q9NTR8.		
DT	01-OCT-2000 (Rel. 40, Created)		
DT	01-OCT-2000 (Rel. 40, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	TUMOR PROTEIN P73 (P53-LIKE TRANSCRIPTION FACTOR) (P53-RELATED PROTEIN).		
GN	TP73 OR P73.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eularchia; Primates; Carnivora; Hominoidea; Homo.		
OX	NCBI_TaxID=9606;		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).		
RC	TISSUE=Colon;		
RX	MEDLINE=97433090; PubMed=9288759;		
RA	Kaghad A., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,		
RA	Minty A., Chalton P., Lelias J.-M., Dumont X., Ferrara P., McKeen F.,		
RA	Caput D.;		
RT	"Monoclonally expressed gene related to p53 at 1p36, a region		
RT	frequently deleted in neuroblastoma and other human cancers.";		
RL	Cell 90:809-819(1997).		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).		
RX	MEDLINE=99289209; PubMed=10362363;		
RA	Yoshikawa H., Negashima M., Khan M.A., McKenamin M.G., Hagihara K.,		
RA	Harris C.C.;		
RT	"Mutational analysis of p73 and p53 in human cancer cell lines.";		
RL	Oncogene 18:3415-3421(1999).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).		
RX	MEDLINE=96389621; PubMed=9721206;		
RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,		
RA	Jenkins R., Smith D.I., Liu W.;		
RT	"Genomic organization and mutation analysis of p73 in		
RT	oligodendrogliomas with chromosome 1 p-arm deletions.";		
RL	Genomics 51:359-363(1998).		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).		
RC	TISSUE=Neuroblastoma;		
RX	MEDLINE=99021697; PubMed=9802988;		
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,		
RA	Anticichiarico-Petruzzelli M., Leviero M., Mellino G.;		
RT	"Two new p73 splice variants, gamma and delta, with different		
RT	transcriptional activity.";		
RL	J. Exp. Med. 188:1763-1768(1998).		
RN	[5]		
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).		
RC	TISSUE=Lymphocytes, Breast cancer, Hepatoma, and Skin;		
RX	MEDLINE=99310936; PubMed=10381648;		
RA	Costanzo A., Leviero M., Knight R.A.;		
RA	"Additional complexity in p73: induction by mitogens in lymphoid cells		
RT	and identification of two new splicing variants epsilon and zeta.";		

RL Cell Death Differ. 6:389-390(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM KAPPA).  
 RA Thomas D.;  
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).  
 RA MEDLINE-99318135; PubMed-10391251.  
 RX Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,  
 RA Kharabanda S., Weichselbaum R., Kufe D.;  
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response  
 to DNA damage.";  
 RL Nature 399:814-817(1999).  
 RN [8]  
 RP ERRATUM.  
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,  
 RA Kharabanda S., Weichselbaum R., Kufe D.;  
 RL Nature 400:792-792(1999).  
 RN [9]  
 RP FUNCTION.  
 RA MEDLINE-99217940; PubMed-10203277;  
 RX Kaelin W.G. Jr.;  
 RA "The emerging p53 gene family.";  
 RL J. Natl. Cancer Inst. 91:594-598(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 439-506.  
 RA MEDLINE-99380160; PubMed-10449409;  
 RX Chi S.W., Ayed A., Arrowsmith C.H.;  
 RT "Solution structure of a conserved C-terminal domain of p73 with  
 structural homology to the SAM domain.";  
 RL EMBL J. 18:4438-4445(1999).  
 CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.  
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE  
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR  
 CC PROTEIN.  
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL  
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY  
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA  
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA  
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- ALTERNATIVE PRODUCTS: 7 ISOFORMS, ALPHA (SHOWN HERE), BETA, GAMMA,  
 CC DELTA, EPSILON, ZETA AND KAPPA. ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING. THE SPLICING OF EXON 11 IN GAMMA AND EPSILON ISOFORMS  
 CC RESULTS IN A FRAMESHIFT FROM THE ORIGINAL READING FRAME. THE  
 CC TO THE ALPHA ISOFORM.  
 CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,  
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.  
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.  
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA  
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS  
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.  
 CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE  
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED  
 CC IN HUMAN CANCERS. IN CONTRAST TO P53, HEMIZYGOSITY IS OBSERVED IN  
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: Y11416; CAA72220.1; -  
 CC EMBL: Y11416; CAA72221.1; -  
 CC EMBL: Y11416; CAA72219.1; -  
 CC EMBL: AF077628; AAC61887.1; -  
 CC EMBL: AF077616; AAC61887.1; JOINED.  
 CC EMBL: AF077617; AAC61887.1; JOINED.

DR EMBL: AF077618; AAC61887.1; JOINED.  
 DR EMBL: AF077619; AAC61887.1; JOINED.  
 DR EMBL: AF077620; AAC61887.1; JOINED.  
 DR EMBL: AF077621; AAC61887.1; JOINED.  
 DR EMBL: AF077624; AAC61887.1; JOINED.  
 DR EMBL: AF077625; AAC61887.1; JOINED.  
 DR EMBL: AF077626; AAC61887.1; JOINED.  
 DR EMBL: AF077627; AAC61887.1; JOINED.  
 DR EMBL: AF079082; AAC61887.1; JOINED.  
 DR EMBL: AF079083; AAC61887.1; JOINED.  
 DR EMBL: AF079084; AAC61887.1; JOINED.  
 DR EMBL: AF079085; AAC61887.1; JOINED.  
 DR EMBL: AF079086; AAC61887.1; JOINED.  
 DR EMBL: AF079087; AAC61887.1; JOINED.  
 DR EMBL: AF079088; AAC61887.1; JOINED.  
 DR EMBL: AF079089; AAC61887.1; JOINED.  
 DR EMBL: AF079091; AAC61887.1; JOINED.  
 DR EMBL: AF079092; AAC61887.1; JOINED.  
 DR EMBL: AF079093; AAC61887.1; JOINED.  
 DR EMBL: AF079094; AAC61887.1; JOINED.  
 DR EMBL: AF079095; AAC61887.1; JOINED.  
 DR EMBL: AF079096; AAC61887.1; JOINED.  
 DR EMBL: AF079097; AAC61887.1; JOINED.  
 DR EMBL: AF079098; AAC61887.1; JOINED.  
 DR EMBL: AF079099; AAC61887.1; JOINED.  
 DR EMBL: AF079100; AAC61887.1; JOINED.  
 DR EMBL: AF079101; AAC61887.1; JOINED.  
 DR EMBL: AF079102; AAC61887.1; JOINED.  
 DR EMBL: AF079103; AAC61887.1; JOINED.  
 DR EMBL: AF079104; AAC61887.1; JOINED.  
 DR EMBL: AF079105; AAC61887.1; JOINED.  
 DR EMBL: AF079106; AAC61887.1; JOINED.  
 DR EMBL: AF079107; AAC61887.1; JOINED.  
 DR EMBL: AF079108; AAC61887.1; JOINED.  
 DR EMBL: AF079109; AAC61887.1; JOINED.  
 DR EMBL: AF079110; AAC61887.1; JOINED.  
 DR EMBL: AF079111; AAC61887.1; JOINED.  
 DR EMBL: AF079112; AAC61887.1; JOINED.  
 DR EMBL: AF079113; AAC61887.1; JOINED.  
 DR EMBL: AF079114; AAC61887.1; JOINED.  
 DR EMBL: AF079115; AAC61887.1; JOINED.  
 DR EMBL: AF079116; AAC61887.1; JOINED.  
 DR EMBL: AF079117; AAC61887.1; JOINED.  
 DR EMBL: AF079118; AAC61887.1; JOINED.  
 DR EMBL: AF079119; AAC61887.1; JOINED.  
 DR EMBL: AF079120; AAC61887.1; JOINED.  
 DR EMBL: AF079121; AAC61887.1; JOINED.  
 DR EMBL: AF079122; AAC61887.1; JOINED.  
 DR EMBL: AF079123; AAC61887.1; JOINED.  
 DR EMBL: AF079124; AAC61887.1; JOINED.  
 DR EMBL: AF079125; AAC61887.1; JOINED.  
 DR EMBL: AF079126; AAC61887.1; JOINED.  
 DR EMBL: AF079127; AAC61887.1; JOINED.  
 DR EMBL: AF079128; AAC61887.1; JOINED.  
 DR EMBL: AF079129; AAC61887.1; JOINED.  
 DR EMBL: AF079130; AAC61887.1; JOINED.  
 DR EMBL: AF079131; AAC61887.1; JOINED.  
 DR EMBL: AF079132; AAC61887.1; JOINED.  
 DR EMBL: AF079133; AAC61887.1; JOINED.  
 DR EMBL: AF079134; AAC61887.1; JOINED.  
 DR EMBL: AF079135; AAC61887.1; JOINED.  
 DR EMBL: AF079136; AAC61887.1; JOINED.  
 DR EMBL: AF079137; AAC61887.1; JOINED.  
 DR EMBL: AF079138; AAC61887.1; JOINED.  
 DR EMBL: AF079139; AAC61887.1; JOINED.  
 DR EMBL: AF079140; AAC61887.1; JOINED.  
 DR EMBL: AF079141; AAC61887.1; JOINED.  
 DR EMBL: AF079142; AAC61887.1; JOINED.  
 DR EMBL: AF079143; AAC61887.1; JOINED.  
 DR EMBL: AF079144; AAC61887.1; JOINED.  
 DR EMBL: AF079145; AAC61887.1; JOINED.  
 DR EMBL: AF079146; AAC61887.1; JOINED.  
 DR EMBL: AF079147; AAC61887.1; JOINED.  
 DR EMBL: AF079148; AAC61887.1; JOINED.  
 DR EMBL: AF079149; AAC61887.1; JOINED.  
 DR EMBL: AF079150; AAC61887.1; JOINED.  
 DR EMBL: AF079151; AAC61887.1; JOINED.  
 DR EMBL: AF079152; AAC61887.1; JOINED.  
 DR EMBL: AF079153; AAC61887.1; JOINED.  
 DR EMBL: AF079154; AAC61887.1; JOINED.  
 DR EMBL: AF079155; AAC61887.1; JOINED.  
 DR EMBL: AF079156; AAC61887.1; JOINED.  
 DR EMBL: AF079157; AAC61887.1; JOINED.  
 DR EMBL: AF079158; AAC61887.1; JOINED.  
 DR EMBL: AF079159; AAC61887.1; JOINED.  
 DR EMBL: AF079160; AAC61887.1; JOINED.  
 DR EMBL: AF079161; AAC61887.1; JOINED.  
 DR EMBL: AF079162; AAC61887.1; JOINED.  
 DR EMBL: AF079163; AAC61887.1; JOINED.  
 DR EMBL: AF079164; AAC61887.1; JOINED.  
 DR EMBL: AF079165; AAC61887.1; JOINED.  
 DR EMBL: AF079166; AAC61887.1; JOINED.  
 DR EMBL: AF079167; AAC61887.1; JOINED.  
 DR EMBL: AF079168; AAC61887.1; JOINED.  
 DR EMBL: AF079169; AAC61887.1; JOINED.  
 DR EMBL: AF079170; AAC61887.1; JOINED.  
 DR EMBL: AF079171; AAC61887.1; JOINED.  
 DR EMBL: AF079172; AAC61887.1; JOINED.  
 DR EMBL: AF079173; AAC61887.1; JOINED.  
 DR EMBL: AF079174; AAC61887.1; JOINED.  
 DR EMBL: AF079175; AAC61887.1; JOINED.  
 DR EMBL: AF079176; AAC61887.1; JOINED.  
 DR EMBL: AF079177; AAC61887.1; JOINED.  
 DR EMBL: AF079178; AAC61887.1; JOINED.  
 DR EMBL: AF079179; AAC61887.1; JOINED.  
 DR EMBL: AF079180; AAC61887.1; JOINED.  
 DR EMBL: AF079181; AAC61887.1; JOINED.  
 DR EMBL: AF079182; AAC61887.1; JOINED.  
 DR EMBL: AF079183; AAC61887.1; JOINED.  
 DR EMBL: AF079184; AAC61887.1; JOINED.  
 DR EMBL: AF079185; AAC61887.1; JOINED.  
 DR EMBL: AF079186; AAC61887.1; JOINED.  
 DR EMBL: AF079187; AAC61887.1; JOINED.  
 DR EMBL: AF079188; AAC61887.1; JOINED.  
 DR EMBL: AF079189; AAC61887.1; JOINED.  
 DR EMBL: AF079190; AAC61887.1; JOINED.  
 DR EMBL: AF079191; AAC61887.1; JOINED.  
 DR EMBL: AF079192; AAC61887.1; JOINED.  
 DR EMBL: AF079193; AAC61887.1; JOINED.  
 DR EMBL: AF079194; AAC61887.1; JOINED.  
 DR EMBL: AF079195; AAC61887.1; JOINED.  
 DR EMBL: AF079196; AAC61887.1; JOINED.  
 DR EMBL: AF079197; AAC61887.1; JOINED.  
 DR EMBL: AF079198; AAC61887.1; JOINED.  
 DR EMBL: AF079199; AAC61887.1; JOINED.  
 DR EMBL: AF079200; AAC61887.1; JOINED.  
 DR EMBL: AF079201; AAC61887.1; JOINED.  
 DR EMBL: AF079202; AAC61887.1; JOINED.  
 DR EMBL: AF079203; AAC61887.1; JOINED.  
 DR EMBL: AF079204; AAC61887.1; JOINED.  
 DR EMBL: AF079205; AAC61887.1; JOINED.  
 DR EMBL: AF079206; AAC61887.1; JOINED.  
 DR EMBL: AF079207; AAC61887.1; JOINED.  
 DR EMBL: AF079208; AAC61887.1; JOINED.  
 DR EMBL: AF079209; AAC61887.1; JOINED.  
 DR EMBL: AF079210; AAC61887.1; JOINED.  
 DR EMBL: AF079211; AAC61887.1; JOINED.  
 DR EMBL: AF079212; AAC61887.1; JOINED.  
 DR EMBL: AF079213; AAC61887.1; JOINED.  
 DR EMBL: AF079214; AAC61887.1; JOINED.  
 DR EMBL: AF079215; AAC61887.1; JOINED.  
 DR EMBL: AF079216; AAC61887.1; JOINED.  
 DR EMBL: AF079217; AAC61887.1; JOINED.  
 DR EMBL: AF079218; AAC61887.1; JOINED.  
 DR EMBL: AF079219; AAC61887.1; JOINED.  
 DR EMBL: AF079220; AAC61887.1; JOINED.  
 DR EMBL: AF079221; AAC61887.1; JOINED.  
 DR EMBL: AF079222; AAC61887.1; JOINED.  
 DR EMBL: AF079223; AAC61887.1; JOINED.  
 DR EMBL: AF079224; AAC61887.1; JOINED.  
 DR EMBL: AF079225; AAC61887.1; JOINED.  
 DR EMBL: AF079226; AAC61887.1; JOINED.  
 DR EMBL: AF079227; AAC61887.1; JOINED.  
 DR EMBL: AF079228; AAC61887.1; JOINED.  
 DR EMBL: AF079229; AAC61887.1; JOINED.  
 DR EMBL: AF079230; AAC61887.1; JOINED.  
 DR EMBL: AF079231; AAC61887.1; JOINED.  
 DR EMBL: AF079232; AAC61887.1; JOINED.  
 DR EMBL: AF079233; AAC61887.1; JOINED.  
 DR EMBL: AF079234; AAC61887.1; JOINED.  
 DR EMBL: AF079235; AAC61887.1; JOINED.  
 DR EMBL: AF079236; AAC61887.1; JOINED.  
 DR EMBL: AF079237; AAC61887.1; JOINED.  
 DR EMBL: AF079238; AAC61887.1; JOINED.  
 DR EMBL: AF079239; AAC61887.1; JOINED.  
 DR EMBL: AF079240; AAC61887.1; JOINED.  
 DR EMBL: AF079241; AAC61887.1; JOINED.  
 DR EMBL: AF079242; AAC61887.1; JOINED.  
 DR EMBL: AF079243; AAC61887.1; JOINED.  
 DR EMBL: AF079244; AAC61887.1; JOINED.  
 DR EMBL: AF079245; AAC61887.1; JOINED.  
 DR EMBL: AF079246; AAC61887.1; JOINED.  
 DR EMBL: AF079247; AAC61887.1; JOINED.  
 DR EMBL: AF079248; AAC61887.1; JOINED.  
 DR EMBL: AF079249; AAC61887.1; JOINED.  
 DR EMBL: AF079250; AAC61887.1; JOINED.  
 DR EMBL: AF079251; AAC61887.1; JOINED.  
 DR EMBL: AF079252; AAC61887.1; JOINED.  
 DR EMBL: AF079253; AAC61887.1; JOINED.  
 DR EMBL: AF079254; AAC61887.1; JOINED.  
 DR EMBL: AF079255; AAC61887.1; JOINED.  
 DR EMBL: AF079256; AAC61887.1; JOINED.  
 DR EMBL: AF079257; AAC61887.1; JOINED.  
 DR EMBL: AF079258; AAC61887.1; JOINED.  
 DR EMBL: AF079259; AAC61887.1; JOINED.  
 DR EMBL: AF079260; AAC61887.1; JOINED.  
 DR EMBL: AF079261; AAC61887.1; JOINED.  
 DR EMBL: AF079262; AAC61887.1; JOINED.  
 DR EMBL: AF079263; AAC61887.1; JOINED.  
 DR EMBL: AF079264; AAC61887.1; JOINED.  
 DR EMBL: AF079265; AAC61887.1; JOINED.  
 DR EMBL: AF079266; AAC61887.1; JOINED.  
 DR EMBL: AF079267; AAC61887.1; JOINED.  
 DR EMBL: AF079268; AAC61887.1; JOINED.  
 DR EMBL: AF079269; AAC61887.1; JOINED.  
 DR EMBL: AF079270; AAC61887.1; JOINED.  
 DR EMBL: AF079271; AAC61887.1; JOINED.  
 DR EMBL: AF079272; AAC61887.1; JOINED.  
 DR EMBL: AF079273; AAC61887.1; JOINED.  
 DR EMBL: AF079274; AAC61887.1; JOINED.  
 DR EMBL: AF079275; AAC61887.1; JOINED.  
 DR EMBL: AF079276; AAC61887.1; JOINED.  
 DR EMBL: AF079277; AAC61887.1; JOINED.  
 DR EMBL: AF079278; AAC61887.1; JOINED.  
 DR EMBL: AF079279; AAC61887.1; JOINED.  
 DR EMBL: AF079280; AAC61887.1; JOINED.  
 DR EMBL: AF079281; AAC61887.1; JOINED.  
 DR EMBL: AF079282; AAC61887.1; JOINED.  
 DR EMBL: AF079283; AAC61887.1; JOINED.  
 DR EMBL: AF079284; AAC61887.1; JOINED.  
 DR EMBL: AF079285; AAC61887.1; JOINED.  
 DR EMBL: AF079286; AAC61887.1; JOINED.  
 DR EMBL: AF079287; AAC61887.1; JOINED.  
 DR EMBL: AF079288; AAC61887.1; JOINED.  
 DR EMBL: AF079289; AAC61887.1; JOINED.  
 DR EMBL: AF079290; AAC61887.1; JOINED.  
 DR EMBL: AF079291; AAC61887.1; JOINED.  
 DR EMBL: AF079292; AAC61887.1; JOINED.  
 DR EMBL: AF079293; AAC61887.1; JOINED.  
 DR EMBL: AF079294; AAC61887.1; JOINED.  
 DR EMBL: AF079295; AAC61887.1; JOINED.  
 DR EMBL: AF079296; AAC61887.1; JOINED.  
 DR EMBL: AF079297; AAC61887.1; JOINED.  
 DR EMBL: AF079298; AAC61887.1; JOINED.  
 DR EMBL: AF079299; AAC61887.1; JOINED.  
 DR EMBL: AF079300; AAC61887.1; JOINED.  
 DR EMBL: AF079301; AAC61887.1; JOINED.  
 DR EMBL: AF079302; AAC61887.1; JOINED.  
 DR EMBL: AF079303; AAC61887.1; JOINED.  
 DR EMBL: AF079304; AAC61887.1; JOINED.  
 DR EMBL: AF079305; AAC61887.1; JOINED.  
 DR EMBL: AF079306; AAC61887.1; JOINED.  
 DR EMBL: AF079307; AAC61887.1; JOINED.  
 DR EMBL: AF079308; AAC61887.1; JOINED.  
 DR EMBL: AF079309; AAC61887.1; JOINED.  
 DR EMBL: AF079310; AAC61887.1; JOINED.  
 DR EMBL: AF079311; AAC61887.1; JOINED.  
 DR EMBL: AF079312; AAC61887.1; JOINED.  
 DR EMBL: AF079313; AAC61887.1; JOINED.  
 DR EMBL: AF079314; AAC61887.1; JOINED.  
 DR EMBL: AF079315; AAC61887.1; JOINED.  
 DR EMBL: AF079316; AAC61887.1; JOINED.  
 DR EMBL: AF079317; AAC61887.1; JOINED.  
 DR EMBL: AF079318; AAC61887.1; JOINED.  
 DR EMBL: AF079319; AAC61887.1; JOINED.  
 DR EMBL: AF079320; AAC61887.1; JOINED.  
 DR EMBL: AF079321; AAC61887.1; JOINED.  
 DR EMBL: AF079322; AAC61887.1; JOINED.  
 DR EMBL: AF079323; AAC61887.1; JOINED.  
 DR EMBL: AF079324; AAC61887.1; JOINED.  
 DR EMBL: AF079325; AAC61887.1; JOINED.  
 DR EMBL: AF079326; AAC61887.1; JOINED.  
 DR EMBL: AF079327; AAC61887.1; JOINED.  
 DR EMBL: AF079328; AAC61887.1; JOINED.  
 DR EMBL: AF079329; AAC61887.1; JOINED.  
 DR EMBL: AF079330; AAC61887.1; JOINED.  
 DR EMBL: AF079331; AAC61887.1; JOINED.  
 DR EMBL: AF079332; AAC61887.1; JOINED.  
 DR EMBL: AF079333; AAC61887.1; JOINED.  
 DR EMBL: AF079334; AAC61887.1; JOINED.  
 DR EMBL: AF079335; AAC61887.1; JOINED.  
 DR EMBL: AF079336; AAC61887.1; JOINED.  
 DR EMBL: AF079337; AAC61887.1; JOINED.  
 DR EMBL: AF079338; AAC61887.1; JOINED.  
 DR EMBL: AF079339; AAC61887.1; JOINED.  
 DR EMBL: AF079340; AAC61887.1; JOINED.  
 DR EMBL: AF079341; AAC61887.1; JOINED.  
 DR EMBL: AF079342; AAC61887.1; JOINED.  
 DR EMBL: AF079343; AAC61887.1; JOINED.  
 DR EMBL: AF079344; AAC61887.1; JOINED.  
 DR EMBL: AF079345; AAC61887.1; JOINED.  
 DR EMBL: AF079346; AAC61887.1; JOINED.  
 DR EMBL: AF079347; AAC61887.1; JOINED.  
 DR EMBL: AF079348; AAC61887.1; JOINED.  
 DR EMBL: AF079349; AAC61887.1; JOINED.  
 DR EMBL: AF079350; AAC61887.1; JOINED.  
 DR EMBL: AF079351; AAC61887.1; JOINED.  
 DR EMBL: AF079352; AAC61887.1; JOINED.  
 DR EMBL: AF079353; AAC61887.1; JOINED.  
 DR EMBL: AF079354; AAC61887.1; JOINED.  
 DR EMBL: AF079355; AAC61887.1; JOINED.  
 DR EMBL: AF079356; AAC61887.1; JOINED.  
 DR EMBL: AF079357; AAC61887.1; JOINED.  
 DR EMBL: AF079358; AAC61887.1; JOINED.  
 DR EMBL: AF079359; AAC61887.1; JOINED.  
 DR EMBL: AF079360; AAC61887.1; JOINED.  
 DR EMBL: AF079361; AAC61887.1; JOINED.  
 DR EMBL: AF079362; AAC61887.1; JOINED.  
 DR EMBL: AF079363; AAC61887.1; JOINED.  
 DR EMBL: AF079364; AAC61887.1; JOINED.  
 DR EMBL: AF079365; AAC61887.1; JOINED.  
 DR EMBL: AF079366; AAC61887.1; JOINED.  
 DR EMBL: AF079367; AAC61887.1; JOINED.  
 DR EMBL: AF079368; AAC61887.1; JOINED.  
 DR EMBL: AF079369; AAC61887.1; JOINED.  
 DR EMBL: AF079370; AAC61887.1; JOINED.  
 DR EMBL: AF079371; AAC61887.1; JOINED.  
 DR EMBL: AF079372; AAC61887.1; JOINED.  
 DR EMBL: AF079373; AAC61887.1; JOINED.  
 DR EMBL: AF079374; AAC61887.1; JOINED.  
 DR EMBL: AF079375; AAC61887.1; JOINED.  
 DR EMBL: AF079376; AAC61887.1; JOINED.  
 DR EMBL: AF079377; AAC61887.1; JOINED.  
 DR EMBL: AF079378; AAC61887.1; JOINED.  
 DR EMBL: AF079379; AAC61887.1; JOINED.  
 DR EMBL: AF079380; AAC61887.1; JOINED.  
 DR EMBL: AF079381; AAC61887.1; JOINED.  
 DR EMBL: AF079382; AAC61887.1; JOINED.  
 DR EMBL: AF079383; AAC61887.1; JOINED.  
 DR EMBL: AF079384; AAC61887.1; JOINED.  
 DR EMBL: AF079385; AAC61887.1; JOINED.  
 DR EMBL: AF079386; AAC61887.1; JOINED.  
 DR EMBL: AF079387; AAC61887.1; JOINED.  
 DR EMBL: AF079388; AAC61887.1; JOINED.  
 DR EMBL: AF079389; AAC61887.1; JOINED.  
 DR EMBL: AF079390; AAC61887.1; JOINED.  
 DR EMBL: AF079391; AAC61887.1; JOINED.  
 DR EMBL: AF079392; AAC61887.1; JOINED.  
 DR EMBL: AF079393; AAC61887.1; JOINED.  
 DR EMBL: AF079394; AAC61887.1; JOINED.  
 DR EMBL: AF079395; AAC61887.1; JOINED.  
 DR EMBL: AF079396; AAC61887.1; JOINED.  
 DR EMBL: AF079397; AAC61887.1; JOINED.  
 DR EMBL: AF079398; AAC61887.1; JOINED.  
 DR EMBL: AF079399; AAC61887.1; JOINED.  
 DR EMBL: AF079400; AAC61887.1; JOINED.  
 DR EMBL: AF079401; AAC61887.1; JOINED.  
 DR EMBL: AF079402; AAC61887.1; JOINED.  
 DR EMBL: AF079403; AAC61887.1; JOINED.  
 DR EMBL: AF079404; AAC61887.1; JOINED.  
 DR EMBL: AF079405; AAC61887.1; JOINED.  
 DR EMBL: AF079406; AAC61887.1; JOINED.  
 DR EMBL: AF079407; AAC61887.1; JOINED.  
 DR EMBL: AF079408; AAC61887.1; JOINED.  
 DR EMBL: AF079409; AAC61887.1; JOINED.  
 DR EMBL: AF079410; AAC61887.1; JOINED.  
 DR EMBL: AF079411; AAC61887.1; JOINED.  
 DR EMBL: AF079412; AAC61887.1; JOINED.  
 DR EMBL: AF079413; AAC61887.1; JOINED.  
 DR EMBL: AF079414; AAC61887.1; JOINED.  
 DR EMBL: AF079415; AAC61887.1; JOINED.  
 DR EMBL: AF079416; AAC61887.1; JOINED.  
 DR EMBL: AF079417; AAC61887.1; JOINED.  
 DR EMBL: AF079418; AAC61887.1; JOINED.  
 DR EMBL: AF079419; AAC61887.1; JOINED.  
 DR EMBL: AF079420; AAC61887.1; JOINED.  
 DR EMBL: AF079421; AAC61887.1; JOINED.  
 DR EMBL: AF079422; AAC61887.1; JOINED.  
 DR EMBL: AF079423; AAC61887.1; JOINED.  
 DR EMBL: AF079424; AAC61887.1; JOINED.  
 DR EMBL: AF079425; AAC61887.1; JOINED.  
 DR EMBL: AF079426; AAC61887.1; JOINED.  
 DR EMBL: AF079427; AAC61887.1; JOINED.  
 DR EMBL: AF079428; AAC61887.1; JOINED.  
 DR EMBL: AF079429; AAC61887.1; JOINED.  
 DR EMBL: AF079430; AAC61887.1; JOINED.  
 DR EMBL: AF079431; AAC61887.1; JOINED.  
 DR EMBL: AF079432; AAC61887.1; JOINED.  
 DR EMBL: AF079433; AAC61887.1; JOINED.  
 DR EMBL: AF079434; AAC61887.1; JOINED.  
 DR EMBL: AF079435; AAC61887.1; JOINED.  
 DR EMBL: AF079436; AAC61887.1; JOINED.  
 DR EMBL: AF079437; AAC61887.1; JOINED.  
 DR EMBL: AF079438; AAC61887.1; JOINED.  
 DR EMBL: AF079439; AAC61887.1; JOINED.  
 DR EMBL: AF079440; AAC61887.1; JOINED.





```

CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M75145; AAA49605.1; -
DR PIR: JH0631; JH0631.
DR HSSP: P04637; JH0631.
DR InterPro: IPR002117; -
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNABIND 90 281 BY SIMILARITY.
FT FT 325 356 OLIGOMERIZATION.
FT DOMAIN 325 392 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 396 AA; 43966 MW; 8422250765545A1C CRC64;

Query Match 35.6%; Score 847.5; DB 1; Length 396;
Best Local Similarity 45.4%; Pred. No. 1e-56;
Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;

QY 11 LSPVFOHIDFLEQPCVQPIDLNFDPSDGAFTKTEISMDICRMDSLDSPMP 70
DB 12 LQSESFEDL-----KMINLVAVQPERE-----SWV 39
QY 71 QYTNLGLNSMDQIQNGSSSTPYNTDHAQNSVTPAPSAOPS-STPDALS-PSPAIPS 128
DB 40 GYNDF-----MMEAPLQ-----VEFDPSTFEVSKTEPAOPSTSLDTGSPSTVPT 87
QY 129 NTDPGPHSDVFSFOOSSTAKSATMTYSTELKKLYCQIAKTPQIAKWTTPPOGAVIRA 188
DB 88 TSYIPALGQLKELSSSTAKSVTCYSPDLNKLFCQIAKTCPOVIVDHPREAVVRA 147
QY 189 MPYKKAHEVTEVYKRCPHNELSREFNEGOIAPSHLRIVGNSHAQVYEDPTGRQSVL 248
DB 148 LAIYKLSADVAVRRCPIHOSSTENNECP-APRGHLVREBNSORSEYEMEDGNTLRHSVL 206
QY 249 VPEPPOVTEFTYLYNFMNCSGVGMNRRPILITVLETRDGOVGRGCFARICAC 308
DB 207 VPEPPOVSECTYLYNFMNCSGVGMNRRPILITVLETRDGOVGRGCFARICAC 266
QY 309 PGDRKADDSIRKQO---VSDSTKNGDGTKRPRQ-NTHGIGMTSTIKRRS-----PDDE 360
DB 267 PGDRKTEENIKKQOETLETETKTPAOGIKRAKKEASLPAPOGASKTKSSPAVSDDE 326
QY 361 LLYLVYRGRETEYMLKTESLEMOYLPOHTIETVYRQO 399
DB 327 IYTLQIRGEKEYEMLKFNDSLELSELYPVADADKYRQK 365

RESULT 4
P53_BABRU STANDARD; PRT; 369 AA.
AC O96678;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Barbus barbus (Barbel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Barbus.
OX NCBI_TaxID=40830;
RN [1]
RP SEQUENCE FROM N.A.
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND BCL2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF071570; AAD34212.1; -
DR InterPro: IPR002117; -
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNABIND 66 256 BY SIMILARITY.
FT DOMAIN 298 329 OLIGOMERIZATION.
FT DOMAIN 342 365 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 368 368 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2C8A74C304 CRC64;

Query Match 34.4%; Score 819.5; DB 1; Length 369;
Best Local Similarity 51.2%; Pred. No. 1.2e-54;
Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;

QY 84 QIQNGSSSTPYNTDHAQNSV-APSPYAOPSSTPDALS-PSPAIPSTNDYPGPHSDVFS 142
DB 26 ELINDEYLPSSFDPIFNVDLQPOPTSP-----PTASVPVADYDVGEGFRLKGF 77
QY 143 QOSSTAKSATMTYSTELKKLYCQIAKTPQIAKWTTPPOGAVIRAMPVYKKAHEVY 202
DB 78 POSGTAKSVTCYSSDLNKLFCQIAKTCPOVGMVNAVPOGSVIRATAIYKSSHAHEVY 137
QY 203 KCPNHHELSREFNEGOIAPSHLRIVGNSHAQVYEDPTGRQSVLVYPPPOVGTETFT 262
DB 138 RRCPIHKEPTD-GDS-LAPAAHLIRVBGNSRALYREDVNSRHSVYVPEVPOLGSEFTT 195
QY 263 VLYNFMNCSGVGMNRRPILITVLETRDGOVGRGCFARICACGPRKADDSIRK 322
DB 196 VLYNFMNCSGVGMNRRPILITVLETRDGOVGRGCFARICACGPRKADDSIRK 255
QY 323 QOVSDFSTKNGD---GTRKRP-RONTHGIGMTSTIKRR-----SPDELLYLVYRGRETEY 373
DB 256 DQ-----EKTIDKIPSAKRSGLTSDSTSVPRPGSKKAKLSSGSDDEIYTLQVIRGEKEYE 312
QY 374 MLKIKESLEIMOYLPOHTIETVYRQO 399
DB 313 MLKKINDSLSDVVPPEMDRYRQK 338

```

```

RESULT 5
P53_BRAE STANDARD; PRT; 373 AA.
ID P53_BRAE
AC P79734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97344388; PubMed=9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
RT "zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RT expression during embryogenesis.";
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U60804; ABA40617.1; -
DR HSSP; P04637; ITR.
DR ZFIN; ZDB-GENE-990415-32; tp53.
DR InterPro; IPR002117; -
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 70 260 BY SIMILARITY.
FT DOMAIN 301 332 OLIGOMERIZATION.
FT DOMAIN 345 366 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).
SO SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B1EF CRC64;

```

```

Query Match 33.8%; Score 805.5; DB 1; Length 373;
Best Local Similarity 53.9%; Pred. No. 1,4e-53;
Matches 158; Conservative 42; Mismatches 82; Indels 11; Gaps 4;

```

```

QY 112 QPSPFALSPAIQSTVDYRGPSPFVSFOQSTAKSATWTSTELKLYCOIAKCP 171
DB 55 QPST---LPTSTVPEPSDIPGDHGFRRLRQSGTASVCTYSPLDKLCKQIAKCP 110
QY 172 IOIKVMPPPQGAIVRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGN 231

```

```

RESULT 6
P53_ICTPU STANDARD; PRT; 376 AA.
ID P53_ICTPU
AC 093379;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99071979; PubMed=9854815;
RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
RT "Identification and characterization of the tumor suppressor p53 in
RT channel catfish (Ictalurus punctatus).";
RL Comp. Biochem. Physiol. 120B:675-682(1998).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF04967; AAC26824.1; -
DR HSSP; P04637; ITR.
DR InterPro; IPR002117; -
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 77 268 BY SIMILARITY.
FT DOMAIN 303 334 OLIGOMERIZATION.
FT DOMAIN 347 372 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 286 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 375 375 PHOSPHORYLATION (BY SIMILARITY).

```

```

DB 111 VQMVVDVAPPGGQSVYRAATIKKSEHVAEVRRCPHNE-RTPPGDNLAPAGHLIRVEGN 168
QY 232 SHAOYVEDPITGRQSVLVPPEPVGTEFTVLYNMCNSSCGGMNRPILIVTLETR 291
DB 169 QRANVEDNITLRLHSVFEPYAPOLGAEWTVLLNYMCMSSCGGMNRRPILITITLETQ 228
QY 292 DGQVLRGRCFARICACGRRKADEDSIRK-QQVSDSTKGGDCTKRFRONTGION-- 348
DB 229 EGQLGRSRFEVRACACGRRKTEESNFKDQETKMTAKTTGTKSLVNESSATLRP 288
QY 349 --TSIKRRSPDELLYLPVRRGTEYMLTKIKESLEMOYLPQHTIETVYRQO 399
DB 289 EGSKKAKOSSSDEFLTQVARGREYELTKLNSLESDVVPASDAEKYRQK 341

```

SQ SEQUENCE 376 AA; 41989 MW; 1B89CD98DB3289F2 CRC64;

## Query Match

Best Local Similarity 33.6%; Score 800; DB 1; Length 376;  
Matches 164; Conservative 45; Mismatches 94; Indels 20; Gaps 5;

OY 108 SPYAPSPFDLSPSPAPSPNDYDGPSPVSPFOSSSTAKSATWYSTEKLKLYCOIA 167

DB 56 SDMLQPOSS--SSPSTVPIVSDYPLGLINLPLHFOESSGKTSVCTSPDLNKLFCOLA 113

OY 168 KTCPIQIXWTTPPGCAVIRAMPVYKKAHEVYKRCPNHLSREFNEGOIAPSHLIR 227

DB 114 KTCPIVMAVSSPPGSVYKATAYVYKSEHVAEYVRCRPHHERSDSDGP-APRGLHLR 172

OY 228 VEGNSHAQYVEDPITGRSVLVPYEPPOVGEFTVLYLNFPCNSSCGANRRPILITVT 287

DB 173 VEGNSRAVYQEDGNTQANSVVPYPPVQGSOSTVLYLNYNCSSCGANRRPILITIT 232

OY 288 LETRGQVYGRRCFARICACPGDRKADSDSIRKQVSDSTKNGDGTCKRPFQNTHGIC 347

DB 233 LETQGHLLGRTEFEVRCACPGDRKTEESNFKKOQ-EPRTSGKTLTKRSMKDPSPHPE 291

OY 348 MTSIKRRSPDELLYLPRGRETYEMLKIKESLELMQYLPHQTTITRYQOQOQOHL 407

DB 292 ASKSKSNSSDDEITYTLQVRKEKEFEFLKINDGLSDVVPADDEKYRQK----- 343

OY 408 LQKHLISACFRNE---LVEPRR 426

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

DB 344 ----LLSKTCRKRERDGAAGEPKR 362

OY 344 ----LLSKTCRKRERDGAAGEPKR 362

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M36962; AAA49923.1; -

DR EMBL; X05191; CAA28821.1; -

DR EMBL; X77546; CAA54672.1; -

DR EMBL; S68353; AAC60746.1; -

DR PIR; A29376; A29376.

DR HSSP; P04637; IISR.

DR InterPro; IPR002117; -

DR Pfam; PF00870; P53; 1.

DR PRINTS; PR00386; P53SUPPRESSR.

DR PROSITE; PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;

KW Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).

FT DNB\_BIND 76 267 BY SIMILARITY.

FT DOMAIN 300 331 OLIGOMERIZATION.

FT DOMAIN 344 356 BASIC (REPRESSION OF DNA-BINDING).

FT MOD\_RES 281 293 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT CONFLICT 52 52 PHOSPHORYLATION (BY SIMILARITY).

FT CONFLICT 71 71 T->S (IN REF. 2).

FT CONFLICT 296 296 MISSING (IN REF. 2).

FT CONFLICT 296 296 MISSING (IN REF. 2).

SQ SEQUENCE 363 AA; 40692 MW; CE1F3E58F020D74D CRC64;

Query Match 32.6%; Score 777.5; DB 1; Length 363;

Best Local Similarity 42.5%; Pred No. 1.7e-51;

Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

OY 2 SOSQGNFELSPVPOHIDFLEOPT---CSVOPDINFEVDEPSEDGATKIKETISMDCI 57

DB 4 SSETGMDPPLSQOETFEEDLWLSLPDPLQVTCRLDNLIS-EFPDYP-----LAADMT 52

OY 58 RMQDSDLSPMPPQYNYNLILNSMDQIQNGSSSRSPYNTDHAQNSVAPSPVAPSSSTF 117

DB 53 VLQD-----GLMGN-----AVPTVT- 67

OY 118 DALSPSPATPSMTDYPGRHSPVSPFOSSSTAKSATWYSTEKLKLYCOIAKTCPIQIKVM 177

DB 68 -----SCAVPSTDDYAGKYGQLDFOQGTAKSVCTYSPPLNKLFCQAKTQCLAVRVE 122

OY 178 TTPPGCAVIRAMPVYKKAHEVYKRCPNHLSREFNEGOIAPSHLIVEGNSHAQYV 237

DB 123 SPPPGSILRATAYVYKKAHEVYKRCPNHLSREFNEGOIAPSHLIVEGNSHAQYV 181

OY 238 EDPITGRSVLVPYPPVQVGEFTVLYLNFPCNSSCGANRRPILITVLETRDQVIG 297

DB 182 EDVNSGRHSCVCPYEGPVGTECTVLYLNYNCSSCGANRRPILITVLETRDQVIG 241

OY 298 RRCFEARICACPGDRKADSDS-IRKQVSDSTKNGDGTCKRPFQNTHGIC-GLQMSIKRR 354

DB 242 RRCFEVRCACPGDRKADSDS-IRKQVSDSTKNGDGTCKRPFQNTHGIC-GLQMSIKRR 292

OY 355 R---SPDELLYLVRGRRETYEMLKIKESLELMQYLPHQTTI 393

DB 293 LVVVDDEEITFLIRIKGRSRYEMLKIKINDALEQESLDQKVK 334

OY 355 R---SPDELLYLVRGRRETYEMLKIKESLELMQYLPHQTTI 393

DB 293 LVVVDDEEITFLIRIKGRSRYEMLKIKINDALEQESLDQKVK 334

OY 355 R---SPDELLYLVRGRRETYEMLKIKESLELMQYLPHQTTI 393

DB 293 LVVVDDEEITFLIRIKGRSRYEMLKIKINDALEQESLDQKVK 334

OY 355 R---SPDELLYLVRGRRETYEMLKIKESLELMQYLPHQTTI 393

DB 293 LVVVDDEEITFLIRIKGRSRYEMLKIKINDALEQESLDQKVK 334

OY 355 R---SPDELLYLVRGRRETYEMLKIKESLELMQYLPHQTTI 393

DB 293 LVVVDDEEITFLIRIKGRSRYEMLKIKINDALEQESLDQKVK 334

OY 355 R---SPDELLYLVRGRRETYEMLKIKESLELMQYLPHQTTI 393

DB 293 LVVVDDEEITFLIRIKGRSRYEMLKIKINDALEQESLDQKVK 334

OY 355 R---SPDELLYLVRGRRETYEMLKIKESLELMQYLPHQTTI 393

DB 293 LVVVDDEEITFLIRIKGRSRYEMLKIKINDALEQESLDQKVK 334

DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).  
GN TP53 OR P53.  
OS Tetraodon miltus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodon.  
NCBI\_TaxID=94908;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;  
RT "Evolutionary conservancy of p53 gene sequences in fish."  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION (BY SIMILARITY).  
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AF071571; A034213.1; -  
DR InterPro: IPR002117; -  
DR Pfam: PF008070; P53; 1.  
DR PRINTS: PR00386; P53SUPPRESSR.  
DR PROSITE: PS00348; P53; 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNAS\_BIND 86 273 BY SIMILARITY.  
FT DOMAIN 308 337 OLIGOMERIZATION.  
FT DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 367 AA; 41266 MW; ACCIOEEZF59CFD CRC64;

Query Match 32.6%; Score 776; DB 1; Length 367;  
Best Local Similarity 42.6%; Pred. No. 2,2e-51;  
Matches 165; Conservative 53; Mismatches 105; Indels 64; Gaps 7;

QY 11 LSPVFOHIMFLPQICVOPIDINEVDESEGGATKIKISMDICIRMODSDISDPMP 70  
DB 10 LSOPTFOLMNVASAP-----PIS-----TIGTALENEAMP 41  
QY 71 QYTNLGLL-NSMDOIOGSSSTSPYNTDHAONSTAPSPYAOPSSSTDALSPSAITSN 129  
DB 42 AEROMNMCMNDSTFNEALNLP-----EPSSRDGAANSSSTPYVPT 84  
QY 130 TDYGPSPFDVSPFOOSSTAKSATWTSTELKKLYCOLAKTCPIQIKVTPPGCAVIRAM 189  
DB 85 TDYGEGERFKLRFGKSGAKSVTSTYSELNKKLYCOLAKTSLVEVLKDKDPPKCAVIRAT 144  
QY 190 PTVKAEVTVVAKRCRPHHELSTREFNSQIAPPSHLIRVGSNSHAQYVEDPITGRSVLV 249  
DB 145 AIVKTEHVAIVVRRCRPHQ-----NEDSAEHRSHLIRMEGSEBAQYFEDHPTROSQVTV 199

QY 250 PYEPQVQTEFTVLYNPMNCSSCGVGNRRPILITVLETRDQVGLRCFPEARICAP 309  
DB 200 PYEPQVQSEFTTILISCMNCSSCGVGNRRPILITVLETRDQVGLRCFPEARICAP 259  
QY 310 GDRKRADEDSIRKQVSDSTANGDGTGRFRONTHGIQMTSIRKRS-----PDELLY 363  
DB 260 GDRKTEETENSTKMQ-----NDAKDAKRRKSVPTPDSTIKRSKTSASAEEDNNEVYT 312  
QY 364 LPVGRRETEMLTKKESLELMQYLPQ 390  
DB 313 LQIRGRKRYEMLKINDGLLENPK 339  
RESULT 9  
ID P53\_FELCA STANDARD; PRT; 366 AA.  
AC P41685;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).  
GN TP53 OR TP53.  
OS Fells silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph node;  
RA MEDLINE=9433960; PubMed=8056458;  
RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Yoon H.Y.,  
RA Watari T., Gotsuka R., Tsujimoto H., Hasegawa A.;  
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in  
RT hematopoietic tumors."  
RL Int. J. Cancer 58:602-607(1994).  
RN [2]  
RP SEQUENCE OF 34-354 FROM N.A.  
RX MEDLINE=94114699; PubMed=8286534;  
RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Gotsuka R.,  
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;  
RT "Molecular cloning and chromosomal mapping of feline p53 tumor  
RT suppressor gene."  
RL J. Vet. Med. Sci. 55:801-805(1993).  
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION.  
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
CC IN MANY TYPES OF CANCER.  
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: D26608; BAA05653.1; -  
DR EMBL: D16460; BAA03927.1; -  
DR HSSP: P04637; ISAH.  
DR InterPro: IPR002117; -  
DR Pfam: PF008070; P53; 1.

DR PRINTS: PR00386; P53SUPPRESSR.  
DR PROSITE: PS00348; P53: 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNA\_BIND 94 285 BY SIMILARITY.  
FT DOMAIN 318 349 OLIGOMERIZATION.  
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).  
FT CONFLICT 285 285 K -> R (IN REF. 2).  
SQ SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8EB78 CRC64;  
  
Query Match 32.3%; Score 770; DB 1; Length 386;  
Best Local Similarity 42.1%; Pred. No. 6.7e-51;  
Matches 161; Conservative 58; Mismatches 103; Indels 60; Gaps 7;  
  
OY 11 LSPVFOHIMDFLEQICVOPIDLFVDEPSEDGATNKIEISMDICRMQSDLSDEPMP 70  
DB 14 LSGEFTSELMNLPE-----NNVLSSELSSAMNELPSED----- 48  
OY 71 QYTNGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAT 126  
DB 49 -----VANMLDEA-----PDDASGMAVAPAPAPAPAT-----PAPALSWPL 85  
OY 127 -----PSNTDYGPSPFVSFOQSTAKSATWYSTEKLKLYCIATKCPQIKVMTPPPO 182  
DB 86 SSFVPSQCTYGAIGFHLGFGSTAKSVCTYSPPLNKLFQIAKTCVQLWVRSPPPP 145  
OY 183 GAVIRAMPYKKAHVTEVYKRCPNHLSREFNEGOIAPSHLIRVEGSHQYVEDPT 242  
DB 146 GTCVRAAAYKKSEFMEVEVRCPHHERCPDSDG-LAPQHLIRVEGSHQYVEDPT 204  
OY 243 GROSIVPEPPOVGTETVLNFMKNSSCVCGANRRPILITVLETRDGVLRCPCE 302  
DB 205 FRHSVYVPEPPEVSGCTIHTNFMKNSSCVCGANRRPILITVLETRDGVLRCPCE 264  
OY 303 ARICACGRKRAKDEDSIRKQVSDSTKNGDCTKRPFRONTGIDQMTSIRKRSDDDEL 362  
DB 265 VRCACGCRDRTEERFERKRGEPPEPPGSTRKALPST-----SSTPOKKKKPLDGEYF 321  
OY 363 YLPVGRREYEMLKIKESLEL 384  
DB 322 TLQIRGRERFERLELLEL 343  
  
RESULT 10  
P53\_PIG STANDARD; PRT; 386 AA.  
AC 09TUB2;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DE 01-OCT-2000 (Rel. 40, Last annotation update)  
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).  
GN TP53 OR P53.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Burr P.D., Argyre D.J., Reid S.W.J., Nasir L.;  
RT "Nucleotide sequence of the pig p53 tumor suppressor cDNA";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF

CC BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION.  
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
CC IN MANY TYPES OF CANCER.  
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: AF098067; AAF04620.1;  
CC InterPro: IPR002117;  
CC DR Pfam: PF00870; P53: 1.  
DR PRINTS: PR00386; P53SUPPRESSR.  
DR PROSITE: PS00348; P53: 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNA\_BIND 94 285 BY SIMILARITY.  
FT DOMAIN 318 349 OLIGOMERIZATION.  
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 386 AA; 42862 MW; AAC3DB8EBDF55162 CRC64;  
  
Query Match 32.2%; Score 767; DB 1; Length 386;  
Best Local Similarity 38.6%; Pred. No. 1.1e-50;  
Matches 167; Conservative 69; Mismatches 125; Indels 72; Gaps 10;  
  
OY 11 LSPVFOHIMDFLEQICVOPIDLFVDEPSEDGATNKIEISMDICRMQSDLSDEPMP 70  
DB 14 LSGEFTSELMNLPE-----NNVLSSELSSAMNELPSED----- 48  
OY 71 QYTNGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAT 126  
DB 49 -----VTNMLDENPDDASRVAP-----PAPAPAPAPAPATSWPL-----SSFVSOK 93  
OY 131 DYPGPHSEFVSFOQSTAKSATWYSTEKLKLYCIATKCPQIKVMTPPPOGAVIRAMP 190  
DB 94 TYPGSTDFRLGFLHSGTAKSVCTYSPALNKLFQIAKTCVQLWVRSPPPPGTRVRAA 153  
OY 191 YKKAHVTEVYKRCPNHLSREFNEGOIAPSHLIRVEGSHQYVEDPTGRQSYLVP 250  
DB 154 IYKKESEYMEVYVRCPHHERSDVSDG-LAPQHLIRVEGSHQYVEDPTGRQSYLVP 212  
OY 251 YEPVGVTEFTVLNFMKNSSCVCGANRRPILITVLETRDGVLRCPCEARICACG 310  
DB 213 YEPVGVSDCTIHTNFMKNSSCVCGANRRPILITVLETRDGVLRCPCEARICACG 272  
OY 311 RDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTGIDQMTSIRKRSDDDEL 370  
DB 273 RDRTEENFLKKGQSCPEPPPGSTRKALPST-----SSSVQKKKKPLDGEYF 329  
OY 371 TYEMLKIKESLELMQVLPQHTTETVRO--QOQOQOHLQKHLISACRNEIYVPRRET 428  
DB 330 RFEMFRELNALDELKD-----AQTARESGENRAHSHLSK-----KQDS 369  
OY 429 PKQSDVFFRSHK 441  
DB 370 PS-----RHKKP 376  
  
RESULT 11  
P53\_CHICK STANDARD; PRT; 367 AA.  
ID P53\_CHICK

AC P10360;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).  
 GN TP53.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPAFAS;  
 RX MEDLINE=89083584; PubMed=3060861.  
 RA Soussi T.;  
 RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear  
 oncoprotein.";  
 RL Nucleic Acids Res. 16:11383-11383(1988).  
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
 GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
 CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
 TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
 ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
 CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
 ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
 BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
 EXPRESSION (BY SIMILARITY).  
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X13057; CA31456.1; -  
 DR PIR; S02193; S02193.  
 DR HSSP; P04637; ITR.  
 DR InterPro; IPR002117; -  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR PROSITE; PS00348; P53; 1.  
 KM Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KM Nuclear protein; Phosphorylation; Apoptosis.  
 FT DNA\_BIND 1 30 TRANSSCRIPTION ACTIVATION (ACIDIC).  
 FT DOMAIN 87 278 BY SIMILARITY.  
 FT DOMAIN 308 339 OLIGOMERIZATION.  
 FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 292 306 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 367 AA; 40169 MW; FC37D0FDF919566 CRC64;

Query Match 32.18; Score 764.5; DB 1; Length 367;  
 Best Local Similarity 44.68; Pred. No. 1.6e-50;  
 Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

OY 11 LSP-EVFOHIMDELQPCISQVPIDLNFVDEPSFDGATNKIEISMDCIRMDSDLSDDMM 69  
 DB 9 LEPEVFNMDLSMLPY---SMQOL-----PLPEDHSMQWELS---PLESPDPPEPP 54  
 OY 70 PQTNYLGLNLSMDQIOINGSSSTSPYNTDHAQNSVTAPSPAPSPSTFDALSPPAIPSN 129  
 DB 55 PPLPL-----AAAAPPLNPP--TPPRAPSPVVEST 85  
 OY 130 TDYGPSPFSDVSPQOSSTAKSATWTYTELKKLYCQIAKTCPIQIKYVTPPGCAVIRAM 189

DB 86 EDYGDGDFRVEYVAGTAKSVTCTYSPVLNKVYCRLAKPCPVYRVGVAPDPSSSLRAV 145  
 OY 190 PVYKAEHTEVYVRCRPHNELSRFNEGOIAPPSHLIRFEGNSHAOVYEDPTGROSLV 249  
 DB 146 AVYKSEHVAEVYVRCRPHNECGGCTDG-LAPAOHLIRVEGNPQARYHDEDTTKRHVV 204  
 OY 250 PYEPVOGTEFTYLVNFMNCSCVCGMNRRLIYLTETRDGOVLGRCEARICACP 309  
 DB 205 PYEPPEVSGDCTTYLVNFMNCSCMGNNRRPILITLLEPGQQLGRCFEVRVACAP 264  
 OY 310 GRDRKADSDIRKOOVSDSTKNGD--TKRPFONTFHSIQMTSIKRRSPDELLYLPVR 367  
 DB 265 GRDKRIEEENFRK-----RGAGAGVAKRAMSPTEAPEPPK-KRYVLNPDNEIFYQVR 316  
 OY 368 GRETYEMLKIKESLELMQ 386  
 DB 317 GRRREYEMLKIEALQIAE 335  
 RESULT 12  
 P53\_CANFA STANDARD; PRT: 381 AA.  
 AC Q29537; Q9TV78;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).  
 GN TP53 OR P53.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eulalia; Carnivora; Fissipedia; Canidae; Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=98178696; PubMed=9519881;  
 RA Veldhoen N., Milner J.;  
 RT "Isolation of canine p53 cDNA and detailed characterization of the  
 full length canine p53 protein.";  
 RL Oncogene 16:1077-1084(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,  
 RA Wataai T., Hasagawa A., Tsujimoto H.;  
 RT "Alterations of p53 tumor suppressor gene in various spontaneous  
 tumors in the dog.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 25-300 FROM N.A.  
 RC STRAIN=BRAGLE;  
 RX MEDLINE=9532915; PubMed=7600529;  
 RA Kraegel S.A., Pazzl K.A., Madewell B.R.;  
 RT "Sequence analysis of canine p53 in the region of exons 3-8.";  
 RL Cancer Lett. 92:181-186(1995).  
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
 GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
 CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
 TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
 ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
 CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
 ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
 BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
 EXPRESSION.  
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 IN MANY TYPES OF CANCER.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration



```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch.)
CC -----
DR EMBL: AF060514; AAC16909.1;
DR EMBL: AB020761; BAA78379.1;
DR HSSP: S77819; AAB42022.1;
DR InterPro: IPR002117;
DR Pfam: PF00870; P53.1;
DR PRINTS: PR00386; P53SUPPRESSOR.
DR PROSITE: PS00348; P53.1;
KM Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; DNA-binding; Transcription regulation; Apoptosis;
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 89 280 BY SIMILARITY.
FT DOMAIN 313 344 OLIGOMERIZATION.
FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
FT MOD_RES 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 2 4 BCS -> OEP (IN REF. 2).
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA: 42486 MM: 761A718FDC3DA59 CRC64;

Query Match 31.68; Score 753.5; DB 1; Length 381;
Best Local Similarity 41.58; Pred. No. 1.2e-49;
Matches 160; Conservative 55; Mismatches 98; Indels 73; Gaps 9;

OY 11 LSPEVGHIMDFL-EOPICSVQ--PID-----INFDERSEDCATNKIEISMDICR 58
DB 14 LSOEFSELMLPENNVLSSELCPANDELLPESVYVNWLDSDDA----- 60
OY 59 MQSDSLSPMPQYTNINGLNSMDQIQNSSSTSPYNTDHAONSVTAPSPYAOPSSPTD 118
DB 61 -----PMRP-----ATSAVTAGP--AASWPL- 80
OY 119 ALSPPAIPSNNTDYPGPHSPDVSFOOSSTAKSATWTYSELKKLYCOLAKTCPIQIKWT 178
DB 81 -----SSSVSPKTYPCGYGFRGLFGLNSGTAKTWTYISLKLKLCOLAKTCPIVOLWVS 136
OY 179 PPGGAVIRAMPYKKAENHYEVYKRCNHELSREFNEGOIAPSHLIRVEGNSHAQVVE 238
DB 137 PPPPNCVRAAIYKKSSEVTEVYVRCRPHERCSDSDG-LAPQHLIRVEGNSHAKTLD 195
OY 239 DPITGQSVLVPEPQVGTFTTLYNVMCNSCVGGMNRRPILITVLTETRGQVYGR 298
DB 196 DRTTFHSHVVVPEPEVGSQDYTIHYVMCMSSCGMGNRRPILITVLTEDSSGNVYGR 255
OY 299 RCFEARIACGPRDRKADDSIRKQVSDSTKNDGTRKRPRTMTHGIOMTSIKKRSPD 358
DB 256 NSPEVAVACGPRDRKTEENFKKKGECPPPPGSGTKRALPST-----SSSPQKKKPLD 312
OY 359 DELLYLVNGRGRTYEMLIKESLEL 384
DB 313 GEYFTLQIRGRERYEMFNINLEALEL 338

RESULT 13
P53-ORLYA
ID P53-ORLYA STANDARD; PRT; 351 AA.
AC P79820;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

CC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
CC Bclioniformes; Adrianchthyidae; Oryziniinae; Oryzias.
CC NCBI_TaxID=8090;
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE=Liver.
CC MEDLINE=97305153; PubMed=9161419;
CC Krause M.K., Rhodes L.D., van Beneden R.J.;
CC Cloning of the p53 tumor suppressor gene from the Japanese medaka
CC (Oryzias latipes) and evaluation of mutational hotspots in MNNG-
CC exposed fish.
CC Gene 189:101-106(1997).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND P53 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch.)
CC -----
DR EMBL: U57306; AAC60146.1;
DR HSSP: P04637; LYCS.
DR InterPro: IPR002117;
DR Pfam: PF00870; P53.1;
DR PRINTS: PR00386; P53SUPPRESSOR.
DR PROSITE: PS00348; P53.1;
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; DNA-binding; Transcription regulation; Apoptosis;
FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 86 272 BY SIMILARITY.
FT DOMAIN 301 330 OLIGOMERIZATION.
FT DOMAIN 333 349 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 282 294 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 350 350 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 351 AA: 39666 MM: BC6153363568BBA1 CRC64;

Query Match 31.38; Score 746; DB 1; Length 351;
Best Local Similarity 43.18; Pred. No. 3.8e-49;
Matches 163; Conservative 54; Mismatches 91; Indels 70; Gaps 10;

OY 16 FOHIMDFLEOPICGVOPIDINFEVDESEDCATNKIEISMDICRMQSDSLSPMPQYTNL 75
DB 14 FOELMETVYPL--ETLSLPTVNEPTGWS-----VAGDMFLDQDLS----- 54
OY 76 GLNSMDQIQNSSSTSPYNTDHAONSVTAPSPYAOPSSPTDALSPPAIPSNNTDYPG 135
DB 55 -----GFDDKI-----FDIP-----IEVPITNEVNPPTVPTVDYDGS 90
OY 136 HSPDVSFOOSSTAKSATWTYSELKLYCOIAKTCPIQIKWTTPPGGAVIRAMPYKKA 195
DB 91 YELFLRQKSGTAKSVTSYSEFLNKLYCOLAKTSPIEVRSKEPKCALIRAAVYKKT 150
OY 196 EHTTEVYKRCNHELSREFNEGOIAPSHLIRVEGNSHAQVVEPITRGQSVLYVPEPQ 255
DB 151 EHVADVRCRPHQ-----NEDSVEHRSHLIRVEGNSHAQVFEEDPYTKRQSVLYVPEPQ 205
OY 256 VGEFTTLYNVMCNSCVGGMNRRPILITVLTETRGQVYGRGRCFARICACGPRDRKA 315

```



DB 206 PGSEMTTLLSYMCSSCMGMNRRPILITLLET-BGLVLRRCFEYRICACPGDRK 264  
 QY 316 DEDIRKQVSDSKNGDKRPRONTHTGIOMTSIKRRS-----PDDELLLYLPYRG 368  
 DB 265 EESRQKTPK-----KRVTPMT-----SSKRKSHSGEEDNEVEHFVEYVG 310  
 QY 369 RETEMLIKESLELMQ 386  
 DB 311 RERYEFLKINDGELLE 328

RESULT 14  
 P53\_BOVIN  
 ID P53\_BOVIN STANDARD; PRT; 386 AA.  
 AC Q29628;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).  
 GN TP53.  
 OS Bos taurus (Bovine), and Bos indicus (Zebu).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NC NCBL\_TaxID=9913; 9915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Bovine; TISSUE-Liver;  
 RX MEDLINE=95352829; PubMed=7626789;  
 RA Dequiedt F., Kettmann R., Burny A., Williams L.;  
 RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";  
 RL DNA Seq. 5:261-264(1995).  
 RN [2]  
 RP SEQUENCE OF 13-386 FROM N.A.  
 RC SPECIES-Bovine; STRAIN-HOLSTEIN; TISSUE-Thymus;  
 RX MEDLINE=96401400; PubMed=8807776;  
 RA Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;  
 RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";  
 RL Vet. Immunol. Immunopathol. 52:53-63(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-B. indicus; STRAIN-BORAN; TISSUE-Blood;  
 RA Bishop R.P., Goblright E.E.I.;  
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
 CC EXPRESSION.  
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 CC IN MANY TYPES OF CANCER.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X81704; CA557348.1; -;  
 CC EMBL: D49825; BAA08629.1; -;  
 CC EMBL: U7486; AAB51214.1; -;  
 CC HSSP: P04637; IYCR.

DR InterPro: IPR002117; -;  
 DR Pfam: PF00870; P53; 1.  
 DR PRINTS: PR00386; P53SUPPRESSR.  
 DR PROSITE: PS00348; P53; 1.  
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DNA\_BIND 94 285 BY SIMILARITY.  
 FT DOMAIN 318 349 OLIGOMERIZATION.  
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 380 380 R -> T (IN REF. 2).  
 SQ SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC64;

Query Match 31.1%; Score 741.5; DB 1; Length 386;  
 Best Local Similarity 38.4%; Pred. No. 9,4e-49;  
 Matches 165; Conservative 68; Mismatches 126; Indels 71; Caps 11;

QY 11 LSPVEQHIWFLQPIGVOPIDNPFVDESEGGATKIKIISMDICRMQSDLSDPMP 70  
 DB 14 LSOETFSDLWMLPEN-----NLSSLSAPVDD 42  
 QY 71 QYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSTPDALSPPA----- 125  
 DB 43 LLPYTDVATWIDECNEAPQMPER-----SAPAAPPAT-----PARATSNPL 85  
 QY 126 ---IPSNIDYEPHPSFDVSSFOSSSTAKSATWYSTELKKLYCQIAKTCPIQIKYMTPEPQ 182  
 DB 86 SSFVPSQKTYGNGVFRGLQSGTAKSVCTYPSLNLKLCQIAKTCPIQVLDWDSPPPP 145  
 QY 183 GAVIRAMPYVKAHEVYVKRCPHNELSRFNEGQIAPSHLRVGSNSIAQYVEDPIT 242  
 DB 146 GTRVRAVAIYKLEHMEVVRCPHERSSDSG-LAPQHLIRVEENLAEYLDQNT 204  
 QY 243 GRSVLVYEPPOVGTETVLYNPMNCSSCVGGMNRRPILITLLETFRDQVGRRCFE 302  
 DB 205 FRHSVYVYEPSEIDSETTIHYNFMNCSSCMGMNRRPILITLLETSCNLLGRNSFE 264  
 QY 303 ARICACPGDRKADSDIRKQVSDSTKNGDKRPRONTHTGIOMTSIKRRSP-DDEL 361  
 DB 265 VRVACPGDRDRTEENLRKKGQSCPEPPRSTKRALPTNT-----SSSPQKKKPLDGEY 320  
 QY 362 LYLVRGRETETMLIKESLELMQYLPQHTIETVYRQOOQOH-QHLLQKLLS-ACERN 419  
 DB 321 FTLDIRGKRYEMRELDALEL-----KDALDREPEGRSHSLKSKRPPSCHKK 375  
 QY 420 ELVPRRRETP 429  
 DB 376 PML--KREGP 383

RESULT 15  
 P53\_MARMO  
 ID P53\_MARMO STANDARD; PRT; 391 AA.  
 AC Q36006;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).  
 GN TP53.  
 OS Marmota monax (Woodchuck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC Mammalia.  
 NC NCBL\_TaxID=9995;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97376996; PubMed=9233767;  
 RA Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;  
 RT "Partial characterization of the woodchuck tumor suppressor, p53, and  
 its interaction with woodchuck hepatitis virus x antigen in

RT hepatocarcinogenesis.";  
RL Oncogene 15:327-336(1997).  
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION.  
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
CC IN MANY TYPES OF CANCER.  
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: AJ001022; CAA04478.1; -  
DR HSSP: P04637; ITRSR.  
DR InterPro: IPR002117; -  
DR Pfam: PF00870; P53; 1.  
DR PRINTS: PR00386; P53SUPPRESSR.  
DR PROSITE: PS00348; P53; 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation.  
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
FT DNA\_BIND 100 290 BY SIMILARITY.  
FT DOMAIN 323 354 OLIGOMERIZATION.  
FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).  
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT MOD\_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).  
SQ SEQUENCE 391 AA; 43468 MW; EIDESDBR4BA0182 CRC64;  
  
Query Match 30.9%; Score 736; DB 1; Length 391;  
Best Local Similarity 38.0%; Pred. No. 2.5e-48;  
Matches 164; Conservative 68; Mismatches 130; Indels 70; Gaps 9;  
  
QY 11 LSPYFQHIWFLQPICSVQPIDLNFVDEPSEGGATNKIEISMDCI RMQSDLSDPMP 70  
DB 14 LQETFFSLMNLTP-----ENNVLSPVLS 38  
QY 71 QYTNGLLNSMDQIONGSSSTSPYNDHAQNSYTAAPSYPQSPSTFALSPSA----- 125  
DB 39 PMDL-LIISFD--VENKFDK---GPEALQMSAAPAPKAPTAPASTLAAPSPATSMPL 91  
QY 126 ---IPSNIDYGPSPHSDVSPFOSSSTANSATWTYSTELKILYCOIAKTCPIQIKWTPPQ 182  
DB 92 SSVPSQNTYPGVYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQIAKTCPIQVQLWVDSITPP 151  
QY 183 GAVIRAMPVYKKAHVYVYKRCNPNHLSREFNNGQIAPSHLIRVGNSHAQYVEDPIT 242  
DB 152 GTRVRAAIAIKKSQHMTEVARCPNHE--RCSDSGLAPQHLIRVEGNLRAEYLDLDRNT 209  
QY 243 GRSVLVPEPPQGTETFTVLYNFMCNSSCVGMNRRPILITVLETRDQVYGRCFE 302  
DB 210 FRHSVVVPIPEPEVSECTIHYNYMCNNSCGMGNRRPILITITLEGSSGNLGRNSFE 269  
QY 303 ARICACGPRKKADEDIRKQVSDSTKNGDGRPRFRONT-----HGIQWTSIKRRSP 357  
DB 270 VRYVACGPRDRTEENFRKR-----GRCPEPPRRTKRALPNCJSSSPQPKKPL 321  
QY 358 DDELLIYVKGRETYEMLIKESLELMQYLPQHTIETVROQOQOQHLLQKHLISACF 417

DB 322 DGEYTLKIRGARFEMFOELNEALDKDAQAEK-----EPGESRPHPSYLSKRGOSTS 376  
QY 418 RNELVEPRREP 429  
DB 377 RHKKIIFRREGP 388

Search completed: August 8, 2001, 01:42:11  
Job time: 390 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 8, 2001, 01:36:50 ; Search time 85.05 Seconds

(without alignments)  
696.915 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 2383  
Sequence: 1 MSQSTQTNFELSPVEVQHIM.....PKQSDVFRHRSKPPNRSVYP 448Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_16:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.phage:\*  
11: sp.plant:\*  
12: sp.spodent:\*  
13: sp.unclassified:\*  
14: sp.vertebrate:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2383	100.0	448	076078	076078 homo sapien
2	2383	100.0	487	09H3D2	09H3d2 homo sapien
3	2296	96.3	483	11_088897	088897 mus musculu
4	2185	91.7	471	4_029PH7	029ph7 homo sapien
5	2185	91.7	516	4_09UP27	09up27 homo sapien
6	2185	91.7	516	4_09P1B7	09p1b7 homo sapien
7	2185	91.7	555	4_09H3D3	09h3d3 homo sapien
8	2185	91.7	641	4_09UP28	09up28 homo sapien
9	2185	91.7	641	4_075195	075195 homo sapien
10	2185	91.7	680	4_09UE10	09ue10 homo sapien
11	2185	91.7	680	4_09H3D4	09h3d4 homo sapien
12	2169	91.0	555	11_09QW20	09qw20 mus musculu
13	2169	91.0	680	11_088898	088898 mus musculu
14	2169	91.0	680	11_09JJP6	09jjp6 mus musculu
15	2011	84.4	393	4_075922	075922 homo sapien
16	1938	81.3	389	11_088899	088899 mus musculu
17	1813	76.1	416	4_09P1B6	09p1b6 homo sapien
18	1813	76.1	461	4_09P1B5	09p1b5 homo sapien
19	1813	76.1	461	4_09UP26	09up26 homo sapien

20	1813	76.1	586	4_09P1B4	09p1b4 homo sapien
21	1813	76.1	586	4_09UBV9	09ubv9 homo sapien
22	1811	76.0	461	11_089WY9	09w9y9 mus musculu
23	1811	76.0	586	11_089097	089097 mus musculu
24	1796	75.4	356	4_09UP74	09up74 homo sapien
25	1796	75.4	586	4_075080	075080 homo sapien
26	1744	73.2	582	13_09DEC7	09dec7 gallus galli
27	1363	57.2	501	4_09H3P8	09h3p8 homo sapien
28	1326.5	55.7	641	13_09M664	09m664 barbus barb
29	1304	54.7	631	11_09JJP2	09jjp2 mus musculu
30	1271.5	53.4	590	11_09JJP1	09jjp1 mus musculu
31	983	41.3	497	11_09W0J0	09w0j0 mus musculu
32	860.5	36.1	621	5_09NGC7	09ngc7 mya arenari
33	853	35.8	443	5_09NGC8	09ngc8 mya arenari
34	746.5	31.3	352	13_09NSU8	09nsu8 oryzae lat
35	746.5	31.3	352	13_09PSU7	09psu7 oryzae lat
36	745.5	31.3	364	5_027937	027937 loligo forb
37	735.5	30.9	387	6_09N252	09n252 sus scrofa
38	732.5	30.7	265	13_09W681	09w681 oncorhynch
39	728.5	30.6	265	13_09W682	09w682 oncorhynch
40	725.5	30.4	265	13_09W680	09w680 oncorhynch
41	723.5	30.4	378	14_P89002	p89002 mastomys na
42	717.5	30.1	393	4_09HA08	09ha08 homo sapien
43	716.5	30.1	393	4_016811	016811 homo sapien
44	714	30.0	390	11_070366	070366 mus musculu
45	713.5	29.9	393	4_015087	015087 homo sapien

## ALIGNMENTS

RESULT 1  
ID 076078 PRELIMINARY; PRT; 448 AA.  
AC 076078;  
DT 01-NOV-1998 (TRENBLER, 08, Created)  
DT 01-NOV-1998 (TRENBLER, 08, Last sequence update)  
DT 01-MAR-2001 (TRENBLER, 16, Last annotation update)  
DE P51 ISOFORM TAP63GAMMA (TA P53 GAMMA).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98448095; PubMed=9774969;  
RA Yang A., Kagnad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,  
RA Caput D., McKeon F.;  
RT "p53, a p53 homolog at 3q27-29, encodes multiple products with  
RT transactivating, death-inducing, and dominant-negative activities.";  
RL Mol. Cell 2:305-316(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SKLETERAL MUSCLE;  
RX MEDLINE=98324755; PubMed=9662378;  
RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,  
RA Ikawa Y., Nimura Y., Nakagawara A., Ohnata M., Ikawa S.;  
RT "Cloning and functional analysis of human p51, which structurally and  
RT functionally resembles p53.";  
RL Nat. Med. 4:839-843(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20388515; PubMed=10935472;  
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,  
RA Yokota J.;  
RT "Mutation and expression of the p51 gene in human lung cancer.";  
RL Neoplasia 1:71-79(1999).  
DR EMBL: AF075428; AAC62633.1; -;  
DR EMBL: AB016072; BAA32592.1; -;  
DR EMBL: AF116770; AAF43486.1; -;  
DR EMBL: AF116775; AAF43486.1; JOINED.  
DR EMBL: AF116757; AAF43486.1; JOINED.  
DR EMBL: AF116759; AAF43486.1; JOINED.

DR EMBL: AF116760; AAF43486.1; JOINED.  
 DR EMBL: AF116761; AAF43486.1; JOINED.  
 DR EMBL: AF116762; AAF43486.1; JOINED.  
 DR EMBL: AF116763; AAF43486.1; JOINED.  
 DR EMBL: AF116764; AAF43486.1; JOINED.  
 DR EMBL: AF116765; AAF43486.1; JOINED.  
 DR HSSP: P04637; IYCS.  
 DR InterPro: IPR002117; -  
 DR Pfam: PF00870; P53; 1.  
 DR PRINTS: PR00386; P53SUPPRESSR.  
 DR ProDom: PD002681; -; 1.  
 SO SEQUENCE 448 AA: 50951 MW: A4FF56B8D1E73A6 CRC64;

Query Match 100.0%; Score 2383; DB 4; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-199;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOPIDLNFDVDEPSEDGATNKIEISMDCIRMO 60  
 DB 1 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOPIDLNFDVDEPSEDGATNKIEISMDCIRMO 60  
 OY 61 DSDLSPPMPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
 DB 61 DSDLSPPMPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
 OY 121 SPSPAIPSNTDYPGPHSFVDFVFOOSSTAKSATWTYSTEKLKYCOIAKTCPIQIKVMTTP 180  
 DB 121 SPSPAIPSNTDYPGPHSFVDFVFOOSSTAKSATWTYSTEKLKYCOIAKTCPIQIKVMTTP 180  
 OY 181 PGGAIVTAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHILRVGNSHAQYVEDP 240  
 DB 181 PGGAIVTAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHILRVGNSHAQYVEDP 240  
 OY 241 ITGROSVLVPEPPQVGEFTTLYVNFMCNSSCVGGMNRRPILIIYLTETRDGOVLGRRC 300  
 DB 241 ITGROSVLVPEPPQVGEFTTLYVNFMCNSSCVGGMNRRPILIIYLTETRDGOVLGRRC 300  
 OY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTGRPFRONTHGIOMTSIRKRRSPDDE 360  
 DB 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTGRPFRONTHGIOMTSIRKRRSPDDE 360  
 OY 361 LLYLPVGRRETYEMLTIKESLELMQYLPQHTIETRYRQOOOQHLLQKHLLSACFRNE 420  
 DB 361 LLYLPVGRRETYEMLTIKESLELMQYLPQHTIETRYRQOOOQHLLQKHLLSACFRNE 420  
 OY 421 LVEPRRETPKQSDVFFRHSPKPNRSVYP 448  
 DB 421 LVEPRRETPKQSDVFFRHSPKPNRSVYP 448

RESULT 2  
 O9H3D2 PRELIMINARY; PRT; 487 AA.  
 AC O9H3D2;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 GN TA P63 GAMMA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98448095; PubMed=9774969;  
 RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,  
 RA Andrews N.C., Caput D., McKeeon F.;  
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
 RT transactivating, death-inducing, and dominant-negative activities.";  
 RL Mol. Cell 2:305-316(1998).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Hagivara K., McMenamin M.G., Harris C.C.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF124540; AAG45609.1; -  
 DR EMBL: AF124528; AAG45609.1; JOINED.  
 DR EMBL: AF124529; AAG45609.1; JOINED.  
 DR EMBL: AF124531; AAG45609.1; JOINED.  
 DR EMBL: AF124532; AAG45609.1; JOINED.  
 DR EMBL: AF124533; AAG45609.1; JOINED.  
 DR EMBL: AF124534; AAG45609.1; JOINED.  
 DR EMBL: AF124535; AAG45609.1; JOINED.  
 SO SEQUENCE 487 AA: 55687 MW: 86C6B5BDF2643BD CRC64;

Query Match 100.0%; Score 2383; DB 4; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-199;  
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOPIDLNFDVDEPSEDGATNKIEISMDCIRMO 60  
 DB 40 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOPIDLNFDVDEPSEDGATNKIEISMDCIRMO 99  
 OY 61 DSDLSPPMPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120  
 DB 100 DSDLSPPMPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159  
 OY 121 SPSPAIPSNTDYPGPHSFVDFVFOOSSTAKSATWTYSTEKLKYCOIAKTCPIQIKVMTTP 180  
 DB 160 SPSPAIPSNTDYPGPHSFVDFVFOOSSTAKSATWTYSTEKLKYCOIAKTCPIQIKVMTTP 219  
 OY 181 PGGAIVTAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHILRVGNSHAQYVEDP 240  
 DB 220 PGGAIVTAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHILRVGNSHAQYVEDP 279  
 OY 241 ITGROSVLVPEPPQVGEFTTLYVNFMCNSSCVGGMNRRPILIIYLTETRDGOVLGRRC 300  
 DB 280 ITGROSVLVPEPPQVGEFTTLYVNFMCNSSCVGGMNRRPILIIYLTETRDGOVLGRRC 339  
 OY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTGRPFRONTHGIOMTSIRKRRSPDDE 360  
 DB 340 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTGRPFRONTHGIOMTSIRKRRSPDDE 399  
 OY 361 LLYLPVGRRETYEMLTIKESLELMQYLPQHTIETRYRQOOOQHLLQKHLLSACFRNE 420  
 DB 400 LLYLPVGRRETYEMLTIKESLELMQYLPQHTIETRYRQOOOQHLLQKHLLSACFRNE 459  
 OY 421 LVEPRRETPKQSDVFFRHSPKPNRSVYP 448  
 DB 460 LVEPRRETPKQSDVFFRHSPKPNRSVYP 487

RESULT 3  
 O88897 PRELIMINARY; PRT; 483 AA.  
 AC O88897;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 GN TA-P63 GAMMA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98448095; PubMed=9774969;  
 RA Yang A., Kagnad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,  
 RA Caput D., McKeeon F.;  
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
 RT transactivating, death-inducing, and dominant-negative activities.";  
 RL EMBL: AF075434; AAC62639.1; -  
 DR HSSP: P04637; IYCS.

DR InterPro: IPR002117; .  
 DR Pfam: PF00870; P53; 1.  
 DR PRINTS: PR00386; P53SUPPRESSR.  
 DR PRODOM: PD002681; -. 1  
 SO SEQUENCE 483 AA; 54969 MW; A90ED0C110C50EAD CRC64;

Query Match 96.3%; Score 2296; DB 11; Length 483;  
 Best Local Similarity 96.9%; Pred. No. 3.2e-191;  
 Matches 434; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 MSOSTQTNELFSEVEFOHIMFLEOPICSVOPIDLFNFDSEDEGATKIEISMDICMQ 60  
 D 40 MSOSTQTNELFSEVEFOHIMFLEOPICSVOPIDLFNFDSEDEGATKIEISMDICMQ 99  
 QY 61 DSDLSDPMMQPYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120  
 D 100 DSDLSDPMMQPYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 159  
 QY 121 SPSPAIPSNTDYPGPHSFDSVFSQOSTAKSATWYSTELKLYCOIAKTCPIQIKVMTTP 180  
 D 160 SPSPAIPSNTDYPGPHSFDSVFSQOSTAKSATWYSTELKLYCOIAKTCPIQIKVMTTP 219  
 QY 181 POGAVIRAMPYKKAEHTEVVKRCPNHELREFNEGOIAPPSHLIRVGNSHAQYVEDP 240  
 D 220 POGAVIRAMPYKKAEHTEVVKRCPNHELREFNEGOIAPPSHLIRVGNSHAQYVEDP 279  
 QY 241 ITGROSVLVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRLILIVLTETRDGOVLGRRC 300  
 D 280 ITGROSVLVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRLILIVLTETRDGOVLGRRC 339  
 QY 301 FEARICACPGDRKADSDSIKQOVSSTKNGDGTGRPFRONTGHIQMTSIKRRSPDE 360  
 D 340 FEARICACPGDRKADSDSIKQOVSSTKNGDGTGRPFRONTGHIQMTSIKRRSPDE 395  
 QY 361 LLYLPVGRRETEYMLKIKESLELMQYLPQHTIETYROOQOQHOLKHLSCFNE 420  
 D 396 LLYLPVGRRETEYMLKIKESLELMQYLPQHTIETYROOQOQHOLKHLSCFNE 455  
 QY 421 LVEPRRETPEKOSDVFFRHSKPPNSVYP 448  
 D 456 LVEPRRETPEKOSDVFFRHSKPPNSVYP 483

RESULT 4  
 Q9NP7 PRELIMINARY; PRT; 471 AA.

AC Q9NP7; TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE P51 ISOFORM TAP63DELTA (P51 DELTA PROTEIN).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20388515; PubMed=10935472;  
 RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,  
 RA Yokota J.;  
 RT "Mutation and expression of the p51 gene in human lung cancer.";  
 RL Neoplasia 1:71-79(1999).  
 DR EMBL: AF116771; AAF61624.1; .  
 DR EMBL: AF116769; AAF43489.1; JOINED.  
 DR EMBL: AF116756; AAF43489.1; JOINED.  
 DR EMBL: AF116757; AAF43489.1; JOINED.  
 DR EMBL: AF116759; AAF43489.1; JOINED.  
 DR EMBL: AF116760; AAF43489.1; JOINED.  
 DR EMBL: AF116761; AAF43489.1; JOINED.  
 DR EMBL: AF116762; AAF43489.1; JOINED.  
 DR EMBL: AF116763; AAF43489.1; JOINED.  
 DR EMBL: AF116764; AAF43489.1; JOINED.

DR EMBL: AF116765; AAF43489.1; JOINED.  
 DR EMBL: AF116766; AAF43489.1; JOINED.  
 DR InterPro: IPR002117; .  
 DR Pfam: PF00870; P53; 1.  
 DR PRINTS: PR00386; P53SUPPRESSR.  
 DR PROSITE: PS00348; P53; UNKNOWN 1.  
 SO SEQUENCE 471 AA; 52882 MW; 32EB39798FCICE69 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 471;  
 Best Local Similarity 94.1%; Pred. No. 1.3e-161;  
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSOSTQTNELFSEVEFOHIMFLEOPICSVOPIDLFNFDSEDEGATKIEISMDICMQ 60  
 D 1 MSOSTQTNELFSEVEFOHIMFLEOPICSVOPIDLFNFDSEDEGATKIEISMDICMQ 60  
 QY 61 DSDLSDPMMQPYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120  
 D 61 DSDLSDPMMQPYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120  
 QY 121 SPSPAIPSNTDYPGPHSFDSVFSQOSTAKSATWYSTELKLYCOIAKTCPIQIKVMTTP 180  
 D 121 SPSPAIPSNTDYPGPHSFDSVFSQOSTAKSATWYSTELKLYCOIAKTCPIQIKVMTTP 180  
 QY 181 POGAVIRAMPYKKAEHTEVVKRCPNHELREFNEGOIAPPSHLIRVGNSHAQYVEDP 240  
 D 181 POGAVIRAMPYKKAEHTEVVKRCPNHELREFNEGOIAPPSHLIRVGNSHAQYVEDP 240  
 QY 241 ITGROSVLVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRLILIVLTETRDGOVLGRRC 300  
 D 241 ITGROSVLVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRLILIVLTETRDGOVLGRRC 300  
 QY 301 FEARICACPGDRKADSDSIKQOVSSTKNGDGTGRPFRONTGHIQMTSIKRRSPDE 360  
 D 301 FEARICACPGDRKADSDSIKQOVSSTKNGDGTGRPFRONTGHIQMTSIKRRSPDE 360  
 QY 361 LLYLPVGRRETEYMLKIKESLELMQYLPQHTIETYROOQOQHOLKHLSCFNE 420  
 D 361 LLYLPVGRRETEYMLKIKESLELMQYLPQHTIETYROOQOQHOLKHLSCFNE 420  
 QY 421 LVEPRRETPEKOSDVFFRHSKPP 442  
 D 411 -----QTSIQSPSSYGNSSPP 426

RESULT 5  
 Q9UP27 PRELIMINARY; PRT; 516 AA.

AC Q9UP27; TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE TA P63 BETA.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98448095; PubMed=9774969;  
 RA Yang A., Kaghad M., Wang Y., Gillette E., Fleming M.D., Dotsch V.,  
 RA Andrews N.C., Caput D., McKoon F.;  
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
 RT transactivating, death-inducing, and dominant-negative activities.";  
 RL Mol. Cell 2:305-316(1998).  
 DR EMBL: AF075432; AAC62637.1; .  
 DR HSSP: P04637; IYCS.  
 DR InterPro: IPR002117; .  
 DR Pfam: PF00870; P53; 1.  
 DR PRINTS: PR00386; P53SUPPRESSR.  
 DR PRODOM: PD002681; -. 1.  
 SO SEQUENCE 516 AA; 57697 MW; 075537810C4738B1 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 516;  
 Best Local Similarity 94.1%; Pred. No. 1.5e-181;  
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```

QY 1 MSOSTGTNEFLSEPVQHIWDFLEQICVOPIDLNFDPESEDEGATNKIEISMDCI RMQ 60
DB 1 MSOSTGTNEFLSEPVQHIWDFLEQICVOPIDLNFDPESEDEGATNKIEISMDCI RMQ 60
QY 61 DSDLSPPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
DB 61 DSDLSPPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
QY 121 SPSPAIPSNTDYPGPHSFDFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPSNTDYPGPHSFDFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
QY 181 PGCAVIIRAMPYVYKKAHEHTEYVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PGCAVIIRAMPYVYKKAHEHTEYVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCYGGMNRRPILITVLTETRDQVGLGRRC 300
DB 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCYGGMNRRPILITVLTETRDQVGLGRRC 300
QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDKTRKPPQNTNGIOMTSIKRRSPDDE 360
DB 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDKTRKPPQNTNGIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRGRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLQKHLISACFRNE 420
DB 361 LLYLPVGRGRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLQKHLISACFRNE 420
QY 421 LVEPRRETPKOSDVFHFHRSKP 442
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 6
Q9P1B7 PRELIMINARY: PRT: 516 AA.
AC Q9P1B7:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
P51 ISOFORM TAP63BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RT Neoplasia 1:71-79(1999).
DR EMBL: AF116768; AAF43488.1; JOINED.
DR EMBL: AF116756; AAF43488.1; JOINED.
DR EMBL: AF116757; AAF43488.1; JOINED.
DR EMBL: AF116759; AAF43488.1; JOINED.
DR EMBL: AF116760; AAF43488.1; JOINED.
DR EMBL: AF116761; AAF43488.1; JOINED.
DR EMBL: AF116762; AAF43488.1; JOINED.
DR EMBL: AF116763; AAF43488.1; JOINED.
DR EMBL: AF116764; AAF43488.1; JOINED.
DR EMBL: AF116765; AAF43488.1; JOINED.
DR EMBL: AF116766; AAF43488.1; JOINED.
DR EMBL: AF116767; AAF43488.1; JOINED.
DR InterPro: IPR002117; -.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.

```

DR PROSITE: PS00348; P53; UNKNOWN\_1.  
 SQ SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 516;  
 Best Local Similarity 94.1%; Pred. No. 1.5e-181;  
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```

QY 1 MSOSTGTNEFLSEPVQHIWDFLEQICVOPIDLNFDPESEDEGATNKIEISMDCI RMQ 60
DB 1 MSOSTGTNEFLSEPVQHIWDFLEQICVOPIDLNFDPESEDEGATNKIEISMDCI RMQ 60
QY 61 DSDLSPPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
DB 61 DSDLSPPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
QY 121 SPSPAIPSNTDYPGPHSFDFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPSNTDYPGPHSFDFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
QY 181 PGCAVIIRAMPYVYKKAHEHTEYVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PGCAVIIRAMPYVYKKAHEHTEYVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCYGGMNRRPILITVLTETRDQVGLGRRC 300
DB 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCYGGMNRRPILITVLTETRDQVGLGRRC 300
QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDKTRKPPQNTNGIOMTSIKRRSPDDE 360
DB 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDKTRKPPQNTNGIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRGRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLQKHLISACFRNE 420
DB 361 LLYLPVGRGRETYEMLLKIKESLELMQYLPQHTIETFRQOQOQOHHLQKHLISACFRNE 420
QY 421 LVEPRRETPKOSDVFHFHRSKP 442
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 7
Q9H3D3 PRELIMINARY: PRT: 555 AA.
AC Q9H3D3:
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
TA P63 BETA.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RT Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagihara K., McMenamin M.G., Harris C.C.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF124532; AAG45608.1; JOINED.
DR EMBL: AF124529; AAG45608.1; JOINED.
DR EMBL: AF124531; AAG45608.1; JOINED.
DR EMBL: AF124532; AAG45608.1; JOINED.
DR EMBL: AF124533; AAG45608.1; JOINED.
DR EMBL: AF124534; AAG45608.1; JOINED.

```



DR EMBL: AF124535; AAC45608.1; JOINED.  
 DR EMBL: AF124536; AAC45608.1; JOINED.  
 DR EMBL: AF124537; AAC45608.1; JOINED.  
 SO SEQUENCE 355 AA; 62433 MW; E22874BE7DBABCE CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 555;  
 Best Local Similarity 94.1%; Pred. No. 1.6e-181;

Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

OY 1 MSQSTQTNELFSPVEVQHIWDFLEQIPICVOPIDLFVDEPSESDATNKIEISMDCIRMQ 60  
 DB 1 MSQSTQTNELFSPVEVQHIWDFLEQIPICVOPIDLFVDEPSESDATNKIEISMDCIRMQ 99  
 OY 61 DSDLSDPMMPOYTNGILNSMDQOIONGSSSTSPYNTHAQNSVTAAPSPYAPQSSSTFDAL 120  
 DB 100 DSDLSDPMMPOYTNGILNSMDQOIONGSSSTSPYNTHAQNSVTAAPSPYAPQSSSTFDAL 159  
 OY 121 SPSPAIIPNTDYPGPHSPDVFSQOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180  
 DB 160 SPSPAIIPNTDYPGPHSPDVFSQOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 219  
 OY 181 POGAVIRAMPYKKAHYTEVVKRCRNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240  
 DB 220 POGAVIRAMPYKKAHYTEVVKRCRNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 279  
 OY 241 ITGRQSVLPYEPPOVGEFTTLYLYNFMCNSSCVGGMNRPLLIIVTLETBDGOVLGRRC 300  
 DB 280 ITGRQSVLPYEPPOVGEFTTLYLYNFMCNSSCVGGMNRPLLIIVTLETBDGOVLGRRC 339  
 OY 301 FEARICACPGDRKADDESIKQOYSDSTKNGDGTKRPFROTHGIQMTSIKRRSPDE 360  
 DB 340 FEARICACPGDRKADDESIKQOYSDSTKNGDGTKRPFROTHGIQMTSIKRRSPDE 399  
 OY 361 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIETRYROOQOOHOLLKHLISACFNE 420  
 DB 400 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIETRYROOQOOHOLLKHLISACFNE 449  
 OY 421 LVEPRRETPTKOSDVFRHSKRP 442  
 DB 450 -----QTISQSPSSYGNSSPP 465

RESULT 8  
 ID Q9UP28 PRELIMINARY: PRT: 641 AA.  
 AC Q9UP28  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE TA P63 ALPHA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98448095; PubMed=9774969;  
 RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,  
 RA Andrews N.C., Caput D., McKeon F.;  
 RT "p53, a p53 homolog at 3q27-29, encodes multiple products with  
 RT transactivating, death-inducing, and dominant-negative activities.";  
 RL Mol. Cell 2:305-316(1998).  
 DR EMBL: AF075430; AAC62635.1; -  
 DR HSP: P04637; IYCS.  
 DR InterPro: IPR001660; -  
 DR InterPro: IPR002117; -  
 DR Pfam: PF00870; P53; 1.  
 DR PRINTS: PR00386; P53SUPPRESSR.  
 DR SMART: SM00454; SAM; 1.  
 SO SEQUENCE 641 AA; 72049 MW; 23A25EBAE63F605 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 641;  
 Best Local Similarity 94.1%; Pred. No. 2e-181;  
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

OY 1 MSQSTQTNELFSPVEVQHIWDFLEQIPICVOPIDLFVDEPSESDATNKIEISMDCIRMQ 60  
 DB 1 MSQSTQTNELFSPVEVQHIWDFLEQIPICVOPIDLFVDEPSESDATNKIEISMDCIRMQ 60  
 OY 61 DSDLSDPMMPOYTNGILNSMDQOIONGSSSTSPYNTHAQNSVTAAPSPYAPQSSSTFDAL 120  
 DB 61 DSDLSDPMMPOYTNGILNSMDQOIONGSSSTSPYNTHAQNSVTAAPSPYAPQSSSTFDAL 120  
 OY 121 SPSPAIIPNTDYPGPHSPDVFSQOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180  
 DB 121 SPSPAIIPNTDYPGPHSPDVFSQOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180  
 OY 181 POGAVIRAMPYKKAHYTEVVKRCRNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240  
 DB 181 POGAVIRAMPYKKAHYTEVVKRCRNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240  
 OY 241 ITGRQSVLPYEPPOVGEFTTLYLYNFMCNSSCVGGMNRPLLIIVTLETBDGOVLGRRC 300  
 DB 241 ITGRQSVLPYEPPOVGEFTTLYLYNFMCNSSCVGGMNRPLLIIVTLETBDGOVLGRRC 300  
 OY 301 FEARICACPGDRKADDESIKQOYSDSTKNGDGTKRPFROTHGIQMTSIKRRSPDE 360  
 DB 301 FEARICACPGDRKADDESIKQOYSDSTKNGDGTKRPFROTHGIQMTSIKRRSPDE 360  
 OY 361 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIETRYROOQOOHOLLKHLISACFNE 420  
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQVLPQHTIETRYROOQOOHOLLKHLISACFNE 410  
 OY 421 LVEPRRETPTKOSDVFRHSKRP 442  
 DB 441 -----QTISQSPSSYGNSSPP 426

RESULT 9  
 ID O75195 PRELIMINARY: PRT: 641 AA.  
 AC O75195  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE P51 ISOFORM TAP63ALPHA (P51B PROTEIN).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SKLETTAL MUSCLE.  
 RX MEDLINE=98324755; PubMed=9662378;  
 RA Osada M., Ohba M., Kawahara C., Ishioke C., Kanamaru R., Katoh I.,  
 RA Ikawa Y., Nimura Y., Nakagawara A., Oblinata M.;  
 RT "Cloning and functional analysis of human p51, which structurally and  
 RT functionally resembles p53.";  
 RL Nat. Med. 4:839-844(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20388515; PubMed=10935472;  
 RA Tanli M., Shindzu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,  
 RA Yokota J.;  
 RT "Mutation and expression of the p51 gene in human lung cancer.";  
 RL Neoplasia 1:71-79(1999).  
 DR EMBL: AB016073; BAA32593.1; -  
 DR EMBL: AF116769; AAF43487.1; -  
 DR EMBL: AF116756; AAF43487.1; JOINED.  
 DR EMBL: AF116757; AAF43487.1; JOINED.  
 DR EMBL: AF116759; AAF43487.1; JOINED.  
 DR EMBL: AF116760; AAF43487.1; JOINED.  
 DR EMBL: AF116761; AAF43487.1; JOINED.  
 DR EMBL: AF116762; AAF43487.1; JOINED.



DR EMBL: AF124528; AAC45607.1; JOINED.  
DR EMBL: AF124529; AAC45607.1; JOINED.  
DR EMBL: AF124531; AAC45607.1; JOINED.  
DR EMBL: AF124532; AAC45607.1; JOINED.  
DR EMBL: AF124533; AAC45607.1; JOINED.  
DR EMBL: AF124534; AAC45607.1; JOINED.  
DR EMBL: AF124535; AAC45607.1; JOINED.  
DR EMBL: AF124536; AAC45607.1; JOINED.  
DR EMBL: AF124537; AAC45607.1; JOINED.  
DR EMBL: AF124538; AAC45607.1; JOINED.  
SQ SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 680;  
Best Local Similarity 94.1%; Pred. No. 2,1e-181;

Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEQPICSVOPIDINFVDEPSEDGATNKIEISMDCIRMQ 60  
DB 40 MSOSTOTNEFLSPEVFOHIMDFLEQPICSVOPIDINFVDEPSEDGATNKIEISMDCIRMQ 99  
QY 61 DSDLSDPMPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDAL 120  
DB 100 DSDLSDPMPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDAL 159  
QY 121 SPSPAIPNTDYPGPHSFDFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180  
DB 160 SPSPAIPNTDYPGPHSFDFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219  
QY 181 POGAVIRAMPYKKAHTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240  
DB 220 POGAVIRAMPYKKAHTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 279  
QY 241 ITGRQSVLVPEPPOVGEFTTLYLNFMCNSSCVGMMRRPLLIVTLETBDGQVLGRRC 300  
DB 280 ITGRQSVLVPEPPOVGEFTTLYLNFMCNSSCVGMMRRPLLIVTLETBDGQVLGRRC 339  
QY 301 FEARICACPGDRKRADESIKROQVSDSTKNGDGTGRPFRONTGHIOMTSIKRRSPDE 360  
DB 340 FEARICACPGDRKRADESIKROQVSDSTKNGDGTGRPFRONTGHIOMTSIKRRSPDE 399  
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISACFRNE 420  
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISACFRNE 449  
QY 421 LVEPRRETPOKSDVFFRRSKRP 442  
DB 450 -----QTSIQSPSSYGNSSPP 465

## RESULT 12

ID 09QWZ0 PRELIMINARY; PRT: 555 AA.  
AC 09QWZ0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE TA-P63 BETA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98448095; PubMed=9774969;  
RA Yang A., Kagnad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,  
RA Caput D., McKeon F.;  
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
transactivating, death-inducing, and dominant-negative activities.";  
RL Mol. Cell 2:305-316(1998).  
DR EMBL: AF075435; AAC62640.1; -.  
DR HSSP: P04637; IYCS.  
DR InterPro: IPR002117; -.

DR Pfam: PF00870; P53: 1.  
DR PRINTS: PR00386; P53SUPPRESSR.  
SQ SEQUENCE 555 AA; 62454 MW; 059E034046EB8987 CRC64;

Query Match 91.0%; Score 2169; DB 11; Length 555;  
Best Local Similarity 93.2%; Pred. No. 4e-180;  
Matches 412; Conservative 6; Mismatches 8; Indels 16; Gaps 1;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEQPICSVOPIDINFVDEPSEDGATNKIEISMDCIRMQ 60  
DB 40 MSOSTOTNEFLSPEVFOHIMDFLEQPICSVOPIDINFVDEPSEDGATNKIEISMDCIRMQ 99  
QY 61 DSDLSDPMPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDAL 120  
DB 100 DSDLSDPMPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDAL 159  
QY 121 SPSPAIPNTDYPGPHSFDFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180  
DB 160 SPSPAIPNTDYPGPHSFDFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219  
QY 181 POGAVIRAMPYKKAHTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240  
DB 220 POGAVIRAMPYKKAHTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 279  
QY 241 ITGRQSVLVPEPPOVGEFTTLYLNFMCNSSCVGMMRRPLLIVTLETBDGQVLGRRC 300  
DB 280 ITGRQSVLVPEPPOVGEFTTLYLNFMCNSSCVGMMRRPLLIVTLETBDGQVLGRRC 339  
QY 301 FEARICACPGDRKRADESIKROQVSDSTKNGDGTGRPFRONTGHIOMTSIKRRSPDE 360  
DB 340 FEARICACPGDRKRADESIKROQVSDSTKNGDGTGRPFRONTGHIOMTSIKRRSPDE 399  
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISACFRNE 420  
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISACFRNE 449  
QY 421 LVEPRRETPOKSDVFFRRSKRP 442  
DB 450 -----QTSIQSPSSYGNSSPP 465

## RESULT 13

ID 088898 PRELIMINARY; PRT: 680 AA.  
AC 088898;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE TA-P63 ALPHA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98448095; PubMed=9774969;  
RA Yang A., Kagnad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,  
RA Caput D., McKeon F.;  
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with  
transactivating, death-inducing, and dominant-negative activities.";  
RL Mol. Cell 2:305-316(1998).  
DR EMBL: AF075436; AAC62641.1; -.  
DR HSSP: P04637; IYCS.  
DR InterPro: IPR001660; -.  
DR InterPro: IPR002117; -.  
DR Pfam: PF00870; P53: 1.  
DR PRINTS: PR00386; P53SUPPRESSR.  
DR ProDom: PD002681; - 1.  
DR SMART: SM00454; SAM: 1.  
SQ SEQUENCE 680 AA; 76788 MW; 8DFF0284F247C68A CRC64;

```

Query Match          91.0%; Score 2169; DB 11; Length 680;
Best Local Similarity 93.2%; Pred. No. 5, 2e-180;
Matches 412; Conservative 6; Mismatches 8; Indels 16; Gaps 1;

QY 1 MSQSTQTNFELSPVEVQHIMWDFLEQPICSVOPIDLNFDVDESEDGATNKIETSMDCIRMQ 60
DB 40 MSQSTQSEFLSPVEVQHIMWDFLEQPICSVOPIDLNFDVDESEDGATNKIETSMDCIRMQ 99
QY 61 DSDLDPMMPQYNTNGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPQSSSTFDAL 120
DB 100 DSDLDPMMPQYNTNGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPQSSSTFDAL 159
QY 121 SPSPAIIPSNITDVGPHSPDVSPFOSSSTAKSATWTSTELKTKLYCOIAKTCPIQIKWMP 180
DB 160 SPSPAIIPSNITDVGPHSPDVSPFOSSSTAKSATWTSTELKTKLYCOIAKTCPIQIKWMP 219
QY 181 PGCAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDP 240
DB 220 PGCAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLTETRDGQVLRRC 300
DB 280 ITGRQSVLPYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLTETRDGQVLRRC 339
QY 301 FEARICACGPRDKADEDSIRKQOVSSTKNGDGTKRPRONTGHIQMTSIKRRSPDDE 360
DB 340 FEARICACGPRDKADEDSIRKQOVSSTKNGDGTKRPRONTGHIQMTSIKRRSPDDE 399
QY 361 LLYLPVRGRETEYMLTKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKHLISACFRNE 420
DB 400 LLYLPVRGRETEYMLTKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKHLISACFRNE 449
QY 421 LVEPRRETQKQSDVFEFRHSKPP 442
DB 450 -----QTSMSQSSSYGNSSPP 465

RESULT 14
QYJUP6 PRELIMINARY; PRT: 680 AA.
AC 09JUP6;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE TA2 KET ALPHA.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LINGUAL EPITHELIUM;
MEDLINE=97460723; PubMed=9115105;
RA Schmale H., Bamberger C.;
RT "A novel protein with strong homology to the tumor suppressor p53.";
RL Oncogene 15:1363-1367(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LINGUAL EPITHELIUM;
RA Schmale H.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y10258; CAB88216.1; -
DR InterPro: IPR002117; -
DR Pfam: PF00870; P53; 1.
DR PRINTS: PRO0386; P53SDPRESSR.
DR PROSITE: PS00348; P53; UNKNOWN.1.
SQ SEQUENCE 680 AA; 76760 MW; AC45DAB8B8F61400 CRC64;

```

```

QY 1 MSQSTQTNFELSPVEVQHIMWDFLEQPICSVOPIDLNFDVDESEDGATNKIETSMDCIRMQ 60
DB 40 MSQSTQSEFLSPVEVQHIMWDFLEQPICSVOPIDLNFDVDESEDGATNKIETSMDCIRMQ 99
QY 61 DSDLDPMMPQYNTNGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPQSSSTFDAL 120
DB 100 DSDLDPMMPQYNTNGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPQSSSTFDAL 159
QY 121 SPSPAIIPSNITDVGPHSPDVSPFOSSSTAKSATWTSTELKTKLYCOIAKTCPIQIKWMP 180
DB 160 SPSPAIIPSNITDVGPHSPDVSPFOSSSTAKSATWTSTELKTKLYCOIAKTCPIQIKWMP 219
QY 181 PGCAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDP 240
DB 220 PGCAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLTETRDGQVLRRC 300
DB 280 ITGRQSVLPYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLTETRDGQVLRRC 339
QY 301 FEARICACGPRDKADEDSIRKQOVSSTKNGDGTKRPRONTGHIQMTSIKRRSPDDE 360
DB 340 FEARICACGPRDKADEDSIRKQOVSSTKNGDGTKRPRONTGHIQMTSIKRRSPDDE 399
QY 361 LLYLPVRGRETEYMLTKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKHLISACFRNE 420
DB 400 LLYLPVRGRETEYMLTKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKHLISACFRNE 449
QY 421 LVEPRRETQKQSDVFEFRHSKPP 442
DB 450 -----QTSMSQSSSYGNSSPP 465

RESULT 15
QYJUP6 PRELIMINARY; PRT: 393 AA.
AC 075922;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE P51 ISOFORM DELGAMMA (DN P63 GAMMA).
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC Hagiwara K., McMenamin M.G., Harris C.C.;

```

RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF075429; AAC62634.1; -  
DR EMBL: AF116770; AAF43490.1; -  
DR EMBL: AF116758; AAF43490.1; JOINED.  
DR EMBL: AF116760; AAF43490.1; JOINED.  
DR EMBL: AF116761; AAF43490.1; JOINED.  
DR EMBL: AF116762; AAF43490.1; JOINED.  
DR EMBL: AF116763; AAF43490.1; JOINED.  
DR EMBL: AF116764; AAF43490.1; JOINED.  
DR EMBL: AF116765; AAF43490.1; JOINED.  
DR EMBL: AF124540; AAG45612.1; -  
DR EMBL: AF124530; AAG45612.1; JOINED.  
DR EMBL: AF124531; AAG45612.1; JOINED.  
DR EMBL: AF124532; AAG45612.1; JOINED.  
DR EMBL: AF124533; AAG45612.1; JOINED.  
DR EMBL: AF124534; AAG45612.1; JOINED.  
DR EMBL: AF124535; AAG45612.1; JOINED.  
DR HSSP: P04637; IYCS.  
DR InterPro: IPR002117; -  
DR Pfam: PF00870; P53; 1.  
DR PRINTS: PR00386; P53SUPPRESSR.  
DR PRODOM: PD002681; -; 1.  
SQ SEQUENCE 393 AA; 44658 MW; C6689B83FD701610 CRC64;

Query Match 84.4%; Score 2011; DB 4; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1,4e-166; Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 70 PQTNTLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 129  
DB 15 PQTNTLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 74  
QY 130 TDYRGPHSFVDVFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPGAVIRAM 189  
DB 75 TDYRGPHSFVDVFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPGAVIRAM 134  
QY 190 PVYKAEHVTEVVKRCPNHLSREFNEGQIAPPSHLIVEGNSHAQYVEDPTGROSVLY 249  
DB 135 PVYKAEHVTEVVKRCPNHLSREFNEGQIAPPSHLIVEGNSHAQYVEDPTGROSVLY 194  
QY 250 PYEPPOVGEFTTLYVLYNMCNNSCVGMNRRPILITVLTETRDGOVLGRCFEARIACAP 309  
DB 195 PYEPPOVGEFTTLYVLYNMCNNSCVGMNRRPILITVLTETRDGOVLGRCFEARIACAP 254  
QY 310 GRDKRADDSIRKQOVSDSTKNGDGTAKRPFRONTGHIQMTSIIKRRSPDDELLYLPVGR 369  
DB 255 GRDKRADDSIRKQOVSDSTKNGDGTAKRPFRONTGHIQMTSIIKRRSPDDELLYLPVGR 314  
QY 370 ETYEMLLKIKESLELMQYLPOHTITFYRQOQOQHLLQKHLISACFRNELVEPRRET 429  
DB 315 ETYEMLLKIKESLELMQYLPOHTITFYRQOQOQHLLQKHLISACFRNELVEPRRET 374  
QY 430 KOSDVFFRHSKPPNRSYTP 448  
DB 375 KOSDVFFRHSKPPNRSYTP 393

Search completed: August 8, 2001, 01:44:36  
Job time: 466 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2001, 21:23:00 ; Search time 4864.29 Seconds  
(Without alignments)  
8954.479 Million cell updates/sec

Title: US-09-670-568b-2  
Perfect score: 2816  
Sequence: 1 tcgtgatcatacaagacagt.....gcattctgtttaaagaaa 2816

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 segs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_pi1:\*  
13: gb\_pi2:\*  
14: gb\_pi3:\*  
15: gb\_pi4:\*  
16: em\_ba1:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
26: em\_htg\_hum5:\*  
27: em\_htg\_hum6:\*  
28: em\_htg\_hum7:\*  
29: em\_htg\_hum8:\*  
30: em\_htg\_inv1:\*  
31: em\_htg\_inv2:\*  
32: em\_htg\_other:\*  
33: em\_htg\_rod:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
36: em\_hum3:\*  
37: em\_hum4:\*  
38: em\_hum5:\*  
39: em\_hum6:\*  
40: em\_hum7:\*  
41: em\_in:\*  
42: em\_om:\*  
43: em\_or:\*

44: em\_ov:\*  
45: em\_pat:\*  
46: em\_ph:\*  
47: em\_pi:\*  
48: em\_ro:\*  
49: em\_sts:\*  
50: em\_sy:\*  
51: em\_un:\*  
52: em\_vi:\*  
53: gb\_sts1:\*  
54: gb\_sts2:\*  
55: gb\_sts3:\*  
56: gb\_sy:\*  
57: gb\_un:\*  
58: gb\_vi1:\*  
59: gb\_vi2:\*  
60: gb\_hcg1:\*  
61: gb\_hcg2:\*  
62: gb\_hcg3:\*  
63: gb\_hcg4:\*  
64: gb\_hcg5:\*  
65: gb\_hcg6:\*  
66: gb\_hcg7:\*  
67: gb\_hcg8:\*  
68: gb\_hcg9:\*  
69: gb\_hcg10:\*  
70: gb\_hcg11:\*  
71: gb\_hcg12:\*  
72: gb\_hcg13:\*  
73: gb\_hcg14:\*  
74: gb\_hcg15:\*  
75: gb\_hcg16:\*  
76: gb\_hcg17:\*  
77: gb\_hcg18:\*  
78: gb\_hcg19:\*  
79: gb\_hcg20:\*  
80: gb\_hcg21:\*  
81: gb\_hcg22:\*  
82: gb\_hcg23:\*  
83: gb\_hcg24:\*  
84: gb\_hcg25:\*  
85: gb\_pi1:\*  
86: gb\_pi2:\*  
87: gb\_pi3:\*  
88: gb\_pi4:\*  
89: gb\_pi5:\*  
90: gb\_pi6:\*  
91: gb\_pi7:\*  
92: gb\_pi8:\*  
93: gb\_pi9:\*  
94: gb\_pi10:\*  
95: gb\_pi11:\*  
96: gb\_pi12:\*  
97: gb\_pi13:\*  
98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2816	100.0	2816	85	AB016072 Homo sapi
2	1440	51.1	1516	91	AF116770 Homo sapi
3	1376	48.9	2031	89	AF116771 Homo sapi
4	1376	48.9	2270	85	AB016073 Homo sapi
5	1364	48.4	4846	9	AX009538 Sequence
6	1364	48.4	4849	92	Y16361 Homo sapien
7	1347	47.8	1347	88	AF075428 Homo sapi
8	1232	43.8	1551	88	AF075432 Homo sapi

9	1232	43.8	1926	88	AF075430
10	1219.6	43.3	1452	88	AF075434
11	1166.2	41.4	4991	95	AF075434
12	1153	40.9	1668	94	AF075435
13	1153	40.9	1668	94	AF075435
14	1143.6	40.6	1182	88	AF075429
15	1031.2	36.6	2082	88	AF061512
16	1031.2	36.6	4708	9	AF061512
17	1031.2	36.6	4756	88	AF091627
18	1028.6	36.5	1386	88	AF075433
19	1028.6	36.5	1761	88	AF075431
20	1026.4	36.4	2820	85	AF075437
21	953.4	33.9	180892	72	AC063939
22	951.2	33.8	1170	94	AF075437
23	884.6	31.4	1386	94	AF075438
24	884.6	31.4	1761	94	AF075439
25	884.6	31.4	4669	94	AB010152
26	770.6	27.4	1506	85	AB042841
27	752	26.7	1749	8	AB045224
28	646.6	23.0	1098	8	AF314148
29	479	17.0	970	93	HSP63G13
30	466.8	16.6	1817	9	AF64599
31	466.8	16.6	1870	9	AF64597
32	466.8	16.6	2156	9	AF64586
33	466.8	16.6	2234	97	HSY11416
34	466.4	16.6	1521	9	AF64595
35	466.4	16.6	1764	9	AF64593
36	465.4	16.5	2155	94	MM019235
37	463.8	16.5	2034	9	AF64584
38	463.8	16.5	2874	9	AF64582
39	463.8	16.5	2874	91	CAY11419
40	461.2	16.4	2452	48	MM019234
41	458.6	15.3	2040	8	AF64588
42	440.2	15.6	2214	8	AF043641
43	340.4	12.1	147765	76	AC084060
44	272.4	9.7	2172	8	XELP53A
45	272.4	9.7	2192	8	XLP53R

## ALIGNMENTS

AF075430 Homo sapi  
AF075434 Mus muscu  
Y10258 Rattus norv  
AF075435 Mus muscu  
AF075436 Mus muscu  
AF075429 Mus muscu  
AF061512 Homo sapi  
AF061512 Homo sapi  
AF091627 Sequence  
AF091627 Homo sapi  
AF075433 Homo sapi  
AF075431 Homo sapi  
AB010153 Homo sapi  
AC063939 Homo sapi  
AF075437 Mus muscu  
AF075438 Mus muscu  
AF075439 Mus muscu  
AB010152 Mus muscu  
AB042841 Homo sapi  
AB045224 Gallus ga  
AF314148 Xenopus l  
AF124540 Homo sapi  
AF64599 Sequence 18  
AF64597 Sequence 16  
AF64586 Sequence 5  
Y11416 H.sapiens m  
AF64595 Sequence 14  
AF64593 Sequence 12  
Y19235 Mus muscu  
AF64584 Sequence 3  
AF64582 Sequence 1  
Y11419 C.aethiops  
Y19234 Mus muscu  
AF64588 Sequence 7  
AF043641 Barbap ba  
AC084060 Mus muscu  
M39962 X.laavis p5  
X05191 Xenopus lea

RESULT 1  
LOCUS AB016072 2816 bp mRNA  
DEFINITION Homo sapiens mRNA for p51A, complete cds.  
ACCESSION AB016072  
VERSION AB016072.1 GI:3510327  
KEYWORDS p51A.  
SOURCE Homo sapiens skeletal muscle cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 2816).  
AUTHORS Ikawa,S. and Osada,M.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUL-1998) to the DDBJ/EMBL/Genbank databases.  
Shuntaro Ikawa, Institute of Development, Aging and Cancer,  
Department of Cell Biology, 4-1 Seto-machi, Sendai, Miyagi  
980-8575, Japan (E-mail:sikawa@idac.tohoku.ac.jp,  
Tel:81-22-717-8484, Fax:81-22-717-8488)  
2 (sites)  
Osada,M., Ohta,M., Kawahara,C., Ishioka,C., Kanamaru,R., Kato,I.,  
Ikawa,Y., Nimura,Y., Nakagawa,A., Ohinata,M. and Ikawa,S.  
Cloning and functional analysis of human p51, which structurally  
and functionally resembles p53  
Nat. Med. 4 (7), 839-843 (1998)  
98324755  
FEATURES  
JOURNAL MEDLINE  
SOURCE Location/Qualifiers  
1. 2816  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"

/map="3q28"  
/tissue\_type="skeletal muscle"  
/tissue="1491"  
/product="p51A"  
/codon\_start=1  
/protein\_id="BA032592.1"  
/db\_xref="GI:3510328"  
/translation="MSQSTQNFLESPVPHQITWDFLEQPCISVQPIDNFVDEPSED  
GATNKLEISMDICIRMODSDLSDPMPQYNTMGLNSMDQIQNGSSSTSPYNTDHAON  
SVTAPSPAPQSTFPDALSPPSPALSPSPALSPSPALSPSPALSPSPALSPSPALSP  
KLYQIAKTCPIQIKVMTPEPGAVIRAMPYVKKAEVTEVRCNHELSPEFNGO  
IAPSHLIRVGENSHAOYVEDPTGRGSRVLYPEPVOYGEFTTYVLYNMCSSCVGG  
MNRRLIIVLETROGOVIGRRCFERRICACGRKADESIRKQVSDSTKNDG  
TKRFRONTGIIOWMTSIRKRSRDELLIIPVGRFTEMLIKRKESLQVLLPQHT  
IEYRQOQOHOHLOKHLKLSRCDREILVEPRREPRKOSDVFFRSKPPNRSVYP"

Query Match 100.0%; Score 2816; DB 85; Length 2816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 tcgttgatatacaagacagtgtaagaatgaatttgaaacttcacggtgaccaccc 60  
1 TCGTTGATATCAAGACAGTGAAGAAATGAAATTTGAAACTTCAAGGTGCCACCT 60  
61 acagtgactgcctgaaccttacatccagcgcttcgtagaaccacgactcattcttg 120  
61 ACAGTGACTGCCCTGACCTTACCTTACCTGAGCGTTTCGAGAAACCCAGCTCATTTCTCTGG 120  
121 aaagaagattatcacgcatccacatgctccagagacacacagaaatgaattccctcagt 180  
121 AAAGAAGATTATTAACCATGATCCACCATGATCCACAGCAGCAGCAATGAATTCCTCACT 180  
181 ccagaagtttccaagatatctggtgatttctggaacacctatgltcagttcagccc 240  
181 CCAGAAGTTTCCAGCATATCTGGATTTCTGGAACACCTATATGTTCACTGACGCC 240  
241 attgacttgacttgltgtagaacatcagaagatggtgtagaagaagaagttagatt 300  
241 ATTGACTTGAACTTTGATGATGAACCATGAGAAAGATGAGTGCACAAACAAGATTGAGATT 300  
301 agcatgactggttcgcatgtagcagactgcgaactgcgaatgtagcccatgltgacacagttac 360  
301 AGCATGACTGTTCCGATGCGATGCGAGACTGCGACCTGAGTGAACCCATGTCGCGACAGTAC 360  
361 acgaacctggggctccttgacagacatgtagcagcagatgtagaagatgctctgctcacc 420  
361 ACGAACCCTGGGCTCCTGTAACAGCATGAGCAGCATTCAGAACGGCTCCTCTCCACCC 420  
421 agtccctataacacagacacgacgacgacagacagcgtcacagcgccctgcctacgacag 480  
421 AGTCCCTATTAACACAGACACCGCAGAACAGCCGACGCGGCCCTGCTGACGACAG 480  
481 ccagtgccacctgtagtctctctctcatcacaccgacatccctccacaacgactac 540  
481 CCAGTGCCACCTTGATGATGCTCTCTCTCATTCACCCGCAATCCCTCCACACGACTAC 540  
541 ccagggccgacagatgtagcgtgtccttcagcagatgtagaagcagcgaagtgcggacc 600  
541 CCAGGCCCGACAGTTTGCAGCTGTCTTCCAGCAGTGCAGACCGCAAGTGCAGCCACC 600  
601 tggagcttccacgtgaactgaagaactctactgcgaatltgcaagaatgagacatgcccac 660  
601 TGGAGCTTTCACGTGAAGTGAAGAACTTACGCGCAAAATTCGAAGACATGCCCATC 660  
661 cagatcaagtgtagacccacccctcctcagagagcgttltacggccatgagctgctctac 720  
661 CAGATCAAGTGATGATGACCCACCTCCAGGAGCGTCTTATCCGCGCATGCTGCTTAC 720  
721 aaaaaagctgtagcagtcacaggaagtgtagaagcgtgcccccaacatgagctgagcgt 780  
721 AAAAAAGCTGAGCAGTCACAGGAAGTGtagaagcgtgcccccaacatgagctgagcgt 780



```
Dh 721 AAAAAAGCTGACGACGTCACGAGGTGGTGAAGCGGTGCCCAACCATGACGTAGCCGT 780
Oy 781 gaattcaacgagggagacgatgtccctcctctagtcattgtatctgagtagaaggagacgc 840
Dh 781 GAAATTCACGAGGAGACGATGTCCTCTCTATGTCATTTGATTTCAGATGAGAGGGAACGCG 840
Oy 841 catgcccaagtagtagaagatcccatcacagaagaacagagtgctgctgtagaactatag 900
Dh 841 CATGCCCGATGTATGAGAAGATCCATCAGNAGAGACGATGTGCTGTACCTTATAG 900
Oy 901 ccaccaccaagctgtgactgaatcacaagagctctgttacaattcattatgtlaaagcaat 960
Dh 901 CCACCCACGAGTGGGACACTGAAATTCACGACAGTCTGTACATTTTCATGTATGAACAGCAGT 960
Oy 961 tgtcttggagagatgaacccgcctccaaatttaactgttactctggaacacagagat 1020
Dh 961 TGTCTGGAGGAGATGAACCCGCTGCATATTTTAATCATTTGTTACTGTGGAACAAGAGAT 1020
Oy 1021 gggcaagctccctggcgcgacgctgtcttgaagcccgatctgtcttgcaggaagagac 1080
Dh 1021 GGGCAAGCTCCCTGGGCGCACGCTGCTTTGAGGCCGAGATCTGTGCTGCCAGGAAGAGAC 1080
Oy 1081 aggaagcgagtagaagaatgaatcaagaagcagcaagtttcgcaagtagacaagaacgct 1140
Dh 1081 AGGAAGCGGAGTGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTACAAAGAACGCT 1140
Oy 1141 gatgttcgaagcgcccgcttccctcagacaacacatgttaccgaatgacatccataag 1200
Dh 1141 GATGTGTCGAAGCGCCCGCTTCTGTAGAACACACATGGTATCCAGATACATCATCAAG 1200
Oy 1201 aaagaagatccccaagatgaatgaactgttatacttaaccagtgagggcgctgagactat 1260
Dh 1201 AAAGAGATCCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Oy 1261 gaaatgctgttgaagatcaagaagctccctggaactcagtagcaactcctcagaacaca 1320
Dh 1261 GAAATGCTGTGGAAGATCAAAAGACTCCCTGGAACATGATGATGATGATGATGATGATGATGAT 1320
Oy 1321 atgaaacgtagcaggaacgaacgaacgaacgaacgaacgaacgaacgaacgaacgaacgaac 1380
Dh 1321 ATTGAACGATACAGGACACACACACACACACACACACACACACACACACACACACACACACAC 1380
Oy 1381 ctttcagcgtctcaggaatgaagctgtgtgagcccgagagaagaacatccaaacatct 1440
Dh 1381 CTTTCAGCGCTCTCAGGAATGAGCTGTGTGAGCCCGGAGAGAAATCCAAACAAATCT 1440
Oy 1441 gaagctctctttagaactccaagcccccaaacagatcagtagtaaccatagagccatc 1500
Dh 1441 GAGCTCTCTTTAGACATTCACACGCCCCCAACCGATCAGTACCCATAGAGCCCTATC 1500
Oy 1501 tctatatttaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
Dh 1501 TCTATATTTTATAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
Oy 1561 tgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1620
Dh 1561 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Oy 1621 ccacacagctcaaaagcaaaagccactagttagagaactcttgaaggagactaaacct 1680
Dh 1621 CCCAACGCTCAAAAGGACAAAGCCACTAGTAGAGATCTTTTGAAGGGGACTCAAACT 1680
Oy 1681 ttacaagaagaagatgtcttcgcagagattgtatcctttagacgggcatgtgtgtgtgtgt 1740
Dh 1681 TTACAAAGAGAGATGTTTCTGCGAGATTTTGTATCCTTAGACCGGCCCTTGTGTGTGTGTGTGT 1740
Oy 1741 gaaccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1800
Dh 1741 GAACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800
Oy 1801 gaaaggggcatlaagatgttatttgaagaccccttctgtctctctgtgtgtgtgtgtgtgt 1860
Dh 1801 GAAAGGGGCATTAAGATGTTTATTTGAACCCCTTCTGTCTTCTGTCTTCTTCTTCTTCTTCTTCT 1860
```

---

```
Oy 1861 aattcacaggaagctttagacaggtctcaacttaagatgtctctttaaagaaagag 1920
Dh 1861 AATTACAGGAGAGCTTTGTGACAGGTCTCAACTTAAGATGCTTTTAAAGAAAGAG 1920
Oy 1921 aaaaaagctgttatgtctgtgcatlaagtagtltgaagtagacaggaacatcagtaga 1980
Dh 1921 AAAAAAGTTGTTATGTGTGTCATTAAGTGTAGTGTACAGAGAGACTCAGTACGA 1980
Oy 1981 cccctttaaagctgtgcatgttaataatgtgcaagtagtaagaacgaaggtgtccaagt 2040
Dh 1981 CCTTTTAACTGTGTCAATGAATTAATTAATTCAGTAACTAAGAAACGAAGCTGTCAAGTTC 2040
Oy 2041 taactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2100
Dh 2041 TACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100
Oy 2101 ttgtggaacttgcatattgtgtccctcccaatgtgtgtagtagaacttcttaat 2160
Dh 2101 TTTGTGACAACTTGCAATTAATTTGTGTCTCCCTCATGTGTGATGAGTAAACATTTCTTAAT 2160
Oy 2161 gctgtgtacctgtccctgtgcacgtgtagtgtgcaatgtttagtcaagtttctgtga 2220
Dh 2161 GCTGTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Oy 2221 catgaacccctgggaagacctactcaaaaaaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
Dh 2221 CATGAACCCCTGGAGAGACTCTACTCAAAAAAACGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280
Oy 2281 ctcatcttgtctctttaaagaagaacacacccccaatgaatgtgtgtgtgtgtgtgtgtgtgt 2340
Dh 2281 CTCATTTTGTCTTTTATTAAGAGACAAATCCACCCAGTAATATGTCCTTACGTAGT 2340
Oy 2341 tgttacaatlaacaaagctcaaaatagaatltggaagccctcacaacatctgtgtat 2400
Dh 2341 TGTTTACCATTAATCAAAAGCTCAAAATGAATTTGAACCCCTCTCACAAATCTGTGATTT 2400
Oy 2401 aattgtctaattagagcttctatccctcgaagccctacacataaacaacagacata 2460
Dh 2401 AATTTGCTTAATTAAGAGCTTCTATTCCTCAAGCCTACTACCATTAACCAAGCATATTA 2460
Oy 2461 ctgaactgtctcagtagcatcttagcagaagagacttaagtttgaagtagaactccaagc 2520
Dh 2461 CTGATACTGTGTACAGGCAATTTAGCCAGAGACTTAAGCTTTGAGTAAGTGAATCAAGC 2520
Oy 2521 agaagtgctttaaatacagacccctggagctggaataaagttgaagggtagactact 2580
Dh 2521 AGAGCTGTTAAATCAGCACCTGAGACTGGAATTAAGAATTTGAAGGTAGACTACTT 2580
Oy 2581 tctcttttcttcaaaaagtttagagaatctcgtttcttcttcaatttaaaaacatatt 2640
Dh 2581 TTTCTTTTTTTACCAAAAGTTTAGAGAACTCTGTTTCTTTCCATTTTAAACATATTT 2640
Oy 2641 ttaagatalaagcatalaagaactttaaaaatgttccctccctcactctccacacccag 2700
Dh 2641 TTAAGATATATGACATTAAGACTTTTAAATAATGTCTCCCTCCATTCCTCCACACCCAGT 2700
Oy 2701 caccagacgttatcttctgtccaccaagaagaatgattctgttcatgtgaagctgttgc 2760
Dh 2701 CACAGCACTGTATTTTCTGTCCACCAACAAATGATTTCTGTGTAATGAGACTGTGCTT 2760
Oy 2761 ttgtgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2816
Dh 2761 TTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2816
```

RESULT 2  
F116756s15 1516 bp DNA PRI 16-MAR-2000  
LOCUS F116756s15 1516 bp DNA PRI 16-MAR-2000  
DEFINITION Homo sapiens p51 gene, exon 15 and complete cds, alternatively  
spliced.  
ACCESSION AF116770  
VERSION AF116770.1 GI:7248444

KEYWORDS  
SEGMENT 15 of 15  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Tanl,M., Shimizu,K., Kawahara,C., Kohno,T., Ishimoto,O., Ikawa,S. and Yokota,J.  
TITLE Mutation and expression of the p51 gene in human lung cancer  
JOURNAL Neoplasia 1 (1), 71-79 (1999)  
MEDLINE 20388515  
AUTHORS 2 (bases 1 to 1516)  
TITLE Tanl,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.  
JOURNAL Direct Submission  
REFERENCE Submitted (28-DEC-1998) Biology Division, National Cancer Center Research Institute, 1-1. Tsukiji 5-chome, Chuo-Ku, Tokyo 104-0045, Japan  
FEATURES  
Source Location/Qualifiers  
1. 1516  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/map="3q28"  
join(AFI16756.1:<1..100,AFI16757.1:324..455,  
AFI16759.1:132..387,AFI16760.1:206..392,  
AFI16761.1:314..429,AFI16762.1:318..427,  
AFI16763.1:185..321,AFI16764.1:236..318,  
AFI16765.1:201..337,77..1516)  
/product="p51 isoform TAp63gamma"  
join(AFI16756.1:27..100,AFI16757.1:324..455,  
AFI16759.1:132..387,AFI16760.1:206..392,  
AFI16761.1:314..429,AFI16762.1:318..427,  
AFI16763.1:185..321,AFI16764.1:236..318,  
AFI16765.1:201..337,77..191)  
/note="B(p51A)"  
/codon\_start=1  
/product="p51 isoform TAp63gamma"  
/protein\_id="AAF43486.1"  
/db\_xref="GI:7248445"  
/translation="MSQSTQINELSPVFOHINDFLPQICSVQPIDLNFVDEPSD  
GATNKIETSMDCIRMDSDSDPMPQYTNGLNSMDQIQONSSSTSPYNDHQA  
STAPSPAPQSPSTFDALSPSPAIIPNTDYPGPHSPDVSFOQSTAKSATMYST  
KLYCQIARTCPQIQIKVTPPGAVIRAMPVYKKAHYTEVKKCPNHEISREFNEQ  
IAPSHLIRVEGNSHAQYVEDPIGRSALVYPRPVQYETTVLNFMCNSCVGQ  
NMRBILITVLETRDGOVIGRCFARICACPERDKADESDIRKQVSDSTKNGD  
TKRPRNTHGIOMTSIKKRSPPDELLYPRGRETPEMLIKESLELMQYLP  
IETVROOOOHOHLQKHLKLSACFRELVEPRRETPEKOSDVEFRHSKPPNSVYP"  
join(AFI16758.1:1..517,AFI16759.1:132..387,  
AFI16760.1:206..392,AFI16761.1:314..429,  
AFI16762.1:318..427,AFI16763.1:185..321,  
AFI16764.1:236..318,AFI16765.1:201..337,77..1516)  
/product="p51 isoform delNgamma"  
join(AFI16758.1:477..517,AFI16759.1:132..387,  
AFI16760.1:206..392,AFI16761.1:314..429,  
AFI16762.1:318..427,AFI16763.1:185..321,  
AFI16764.1:236..318,AFI16765.1:201..337,77..191)  
/codon\_start=1  
/product="p51 isoform delNgamma"  
/protein\_id="AAF43490.1"  
/db\_xref="GI:7248449"  
/translation="MLYENNAQTQFSEQYTNLGLNSMDQIQONSSSTSPYNTD  
HONSVPAPSPAPSPSTFDALSPSPAIIPNTDYPGPHSPDVSFOQSTAKSATMYST  
ELKKIQIARTCPQIQIKVTPPGAVIRAMPVYKKAHYTEVKKCPNHEISREFNEQ  
EGQIAPSPHILIRVEGNSHAQYVEDPIGRSALVYPRPVQYETTVLNFMCNSCVG  
VGGIAPSPHILITVLETRDGOVIGRCFARICACPERDKADESDIRKQVSDSTKNG  
GDGTRPFQNTGHIOMTSIKKRSPPDELLYPRGRETPEMLIKESLELMQYLP  
OHTIETVROOOOHOHLQKHLKLSACFRELVEPRRETPEKOSDVEFRHSKPPNSV  
P"

exon  
BASE COUNT 408 a 293 c 313 g 502 t  
ORIGIN

Query Match 51.1%; Score 1440; DB 91; Length 1516;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1377 tctccttcaagctgcttgaagaaatgagctgtggaagcccgagagaaatccaaaca 1436  
DB 77 TCCCTTTAGCCTGCTGCTTGTAGGAATGAGCTGTGTGAGCCCGGAGAAATCCAAACA 136  
QY 1437 acctgacgtctcttcttaagacattccaaagcccccacacagatgtaaccatgaagcc 1496  
DB 137 ACTGACGCTCTCTTTAGACATTCACACCCCAACGATGATGATGATGATGATGATG 196  
QY 1497 tctctctattttaaagt 1556  
DB 197 TATCTATATTTTAAAGT 256  
QY 1557 tgtatgt 1616  
DB 257 TGTATGT 316  
QY 1617 gagaccacactgtctcaaaagcacaagccactagtgagagaatctttgagagactcaa 1676  
DB 317 GAGACCCACACTGCTCAAAAGCCACAAAGCCACACTAGTGAAGAACTTTTGAAGGACTCA 376  
QY 1677 acccttcaaaagagagatgtttctctgagaattgtatactcttagaccgacatgtgtg 1736  
DB 377 ACCCTTCAAAAGAAAGATGTTTCTGCAATTTGTATGCTTAAAGCCGCCATTGGTGCG 436  
QY 1737 tgaaggaacacatgt 1796  
DB 437 TGAGGAACCACTGCTGT 496  
QY 1797 tgggaaagagagcaatgaagtgttcttgaagaccccttctctctctctgtgtgtt 1856  
DB 497 TGGGAAAGGCGCATTAAGATGTTTATTGGAACCTTTCTCTCTCTCTCTCTCTCTCTCT 556  
QY 1857 ctaaatctcaaggaagacttttgaagagcttcaaaacttaagatgtcttttgaagaaa 1916  
DB 557 CTAATAATTCACAGGAAGCTTTTGAACAGCTGTCAAACTTAAGATGCTTTTAAAGAAA 616  
QY 1917 ggaagaaaagagtgatgt 1976  
DB 617 GGAGAAAAAAGTTGTTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 676  
QY 1977 cagaacctttaaagctgt 2036  
DB 677 CAGACCCCTTTAATGCTGT 736  
QY 2037 agtgaactgtcgtgagagagagtgatcaattccaaagtaacttgtgtgtgtgtgtgt 2096  
DB 737 ACTGATCTCTGTGAGGAGGAGGTGATCAATTAAGTAATCAACTTGTGTGTGTGTGTGT 796  
QY 2097 gtctcttgtaagaaatgtcatatattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2156  
DB 797 GTTCTTGTGAGAACTGTGATTAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 856  
QY 2157 taatcttgaacgt 2216  
DB 857 TAATCTGT 916  
QY 2217 tgaatagaagacccctggaagacactacacaaagagtggtgtgtgtgtgtgtgtgtgtgt 2276  
DB 917 TGTATGATGAACCTGTGAGAGACCTACACAAAAAACTGTTGTGTGTGTGTGTGTGTGTGT 976  
QY 2277 tgaactaatgt 2336  
DB 977 TGAACCTATTTTGTGCTTTTAATGAAGAAACAAATCCACCCAGTAATATTCGCCCTTAC 1036  
QY 2337 tagttgttaacattatcaagctcaaaatagaatttgaagccctctcaaaaatctgt 2396  
DB 1037 TAGTTGTTTACATTAATCAAAAGCTCAAAATTAAGATTTGAAGCCCTCTCAAAATCTGT 1096

OY 2397 gattaatctgtaattagagcttctatccctcaagccttaccataaaaccagccat 2456  
|||||  
DB 1097 GATTAAATGGCTTAATATGAGCTTATACCTCAAGCCTACCTACATTAACAGCCAT 1156  
OY 2457 attactgatactgctcagtgacttaagccagagacttcttgtaagtaagtgaatcc 2516  
|||||  
DB 1157 ATTACTGATAGCTGTTCACTGATTTAGCCAGAGACTTACGTTTGAAGTGAATGCC 1216  
OY 2517 aagcagaagtgtaaatcagcactcctcgactggaatlaaagatgaaaggtagact 2576  
|||||  
DB 1217 AAGCAGAGGTGTAAATACACACTCCGACTGGAATTAAGATTAAGAGGTAGACT 1276  
OY 2577 acttctctcttttaccacaaggtttagaagatcctgcttctcttccattttaaaca 2636  
|||||  
DB 1277 ACTTTTCTTTTCTTTTACTCAAAAGTTTGAAGANATCTGTTTCTTCCATTTTAAACA 1336  
OY 2637 taattaaagataagcataaagacttaaaaatgctccctccctcacttccacacac 2696  
|||||  
DB 1337 TATTTTAAGATTAATAGCATTAAGAAAGACTTAAATGTCTCCCTCCATCTTCCACAC 1396  
OY 2697 cagttaccagaactgctatttctctgacaccagaagaatcttctgtcaatggaagctt 2756  
|||||  
DB 1397 CAGTCACGACGACTGATTTCTGTCCACCAAGACATGATTTCTGTATGAGGCTGT 1456  
OY 2757 gctttctggaatgctgacttaattcaattcaacttttgactctggtttaaagaaa 2816  
|||||  
DB 1457 GCTTTTGGATGATGCTGATTTTAAATTTCAATTAACCTTTTGATCTTGTTTAAAGAAA 1516  
  
RESULT 3  
AF116771 AF116771 2031 bp mRNA PRI 02-APR-2000  
LOCUS Homo sapiens p51 delta mRNA, complete cds.  
DEFINITION AF116771  
ACCESSION AF116771.1 GI:7384975  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2031)  
AUTHORS Tanl,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.  
TITLE Mutations and expression of the p51 gene in human lung cancer  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2031)  
AUTHORS Tanl,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-1998) Biology Division, National Cancer Center  
Research Institute, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045,  
Japan  
  
FEATURES  
Source location/Qualifiers  
1..2031  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/map="3q28"  
145..1560  
/note="p53-like"  
/codon\_start=1  
/product="p51 delta"  
/protein\_id="AAF61624.1"  
/db\_xref="GI:7384976"  
/translation="MSOSTQTNFLSPVFOHIDFLPQICSVQPIDLNFVDEPSED  
GATNKIEISMDCIKMODSDLSDPMPOTNIGLNSMDQOIONSSSTSPYNTDHAON  
SVTAPSPYAPDSSTFDALSPSPALPSNDYGPSPFVDSFVQSSSTASATWTSTELK  
KLVCQIAKTCPIQIKVMPPEPGAVIRAMPVYKRAEHVTEFKCPNHELSRENEG  
IAPSHLIRVGNHAYVEDPITGRQSVLVPEYPPQVTEFTVLVNFQMSNCEVG  
MNRBDILIVLTLERDGOVLCRCEPARIKCRDRKADDSIRKQOVSSTKNGDS  
TKRPFQNTHTQMTSTIKKRSPPDELLYLEVRKRETEMLKIKESLEMLQYLPQHT  
IEYRQOQOQHOHLQKQTSIQSPSSYGNSSPPLNKMNSMKNLPSVQLINPOORNA  
LTPPTIDGMGANSRGSSENP"  
  
BASE COUNT 543 a 591 c 454 g 443 t

ORIGIN  
Query Match 48.9%, Score 1376, DB 89; Length 2031;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 tcgtgatatacaagaacagtgtaagaataatttgaacttcaagtggtgcaacct 60  
|||||  
DB 1 TCGTGTATATCAAAAGACAGTTGAAGAAATGATTTTGAACCTTACGGTGCCACCTT 60  
OY 61 acaagtagcccttgacccttaccatccagcgttctgtagaaccacagctcattctctg 120  
|||||  
DB 61 ACAGTAGCGCCCTGACCCCTTACATCCAGGTTTCTAGAAACCCAGTCATTTCTCTGG 120  
OY 121 aaagaagtattaccgatccacatgctccagagacacagacaatargaattcctcagt 180  
|||||  
DB 121 AAAGAAAGTTATATACCGATCCACATGTCGCCAGACACACACAAATGAATTCCTCAGT 180  
OY 181 ccaagagtttccagacatatctgggatttcttgagaagacctatagtctcagtcagccc 240  
|||||  
DB 181 CCAGAGGTTTCCACATATCTGGGATTTTCTGGAACACCTATATGTTCAGTTACGCC 240  
OY 241 attgacttgaacttgytgalgaaccatcaagaatggtgcygacaacaagaattgagatt 300  
|||||  
DB 241 ATTGACTTGAACTTGTGTGATGAACCATCAGAAAGATGTCGACAAACAAATGAGATT 300  
OY 301 agcatggaactgtatctcgcgatcgaggaactcggaactgagtgaccccatgtgccaagatc 360  
|||||  
DB 301 AGCATGGACTGTATCCGATCGCATCGAGACTCGACCTGATGACCCCATGTGGCCACAGTAC 360  
OY 361 acgaacctggggctcctctgaacagacatggaacagagattcagaagggctcctgcacc 420  
|||||  
DB 361 ACGAACCTGGGGCTCCTCTGAACAGCATGACACGACGATTTCAAGAGGCTCCTCTGCCAC 420  
OY 421 agtccctlaaacacagacacacgcgcagaacagcgtcaacgcgcctcgcctacgcagaag 480  
|||||  
DB 421 ACTCCCTATTAACACAGACACACGCGCAGAAACAGCGTACAGGCGCCCTCGCTACGCACAG 480  
OY 481 cccaagctccacttgaatgctctctctcatatcccgccatccctccaaacgcgaatc 540  
|||||  
DB 481 CCCACTCCACCTTGATGAGCTCTCTCATATCACCCTCATCCCTCCAAACGCACTATC 540  
OY 541 ccaggcccgacagtttgcagtgctccttcacagagtcgaagcaccgcgaagtcgcgcacc 600  
|||||  
DB 541 CCAGGCCCGCACAGTTTGCAGCTGCTCTTCCAGCAGTGAGACGCCCAAGTCGGCCAC 600  
OY 601 tggacgtatccactgaactgaagaacttacttgcgaatgtcaaatgtcaaatgacatc 660  
|||||  
DB 601 TGGACGTATTCACGTGAACCTGCTCTGAGGAGCTGTTATCGGGCCATGCTCTCTATC 660  
OY 661 cagatcaaggtgatagaaccacacctcctcaaggagctgttatacgcgcacatgacctc 720  
|||||  
DB 661 CAGATCAAGGTATGACCCACCTCTCTGAGGAGCTGTTATCGGGCCATGCTCTCTATC 720  
OY 721 aaaaaagctgagcaggtcagcaggtgtgtgaaagcgtgtgcccacacatgaagctgagcgt 780  
|||||  
DB 721 AAAAAAGCTGAGCACGCTCACGAGGAGGTGTGAAGCGGTGCCCAACCATGAGCTGAGCGCT 780  
OY 781 gaattcaacgaggaacagattgcccctcctacttcatlgtatcgaatgaaggaggaacag 840  
|||||  
DB 781 GAATTCACGAGGAGGACAGATTGCCCTCTCTACTCATTTGATTCGAGTGAAGGGAACAGC 840  
OY 841 catgcccaatgatagaatcccatcaacaggaagaacagagtgtcgtgttacctatgag 900  
|||||  
DB 841 CATGCCCATGATGTAGAGATCCATCACAGGAACACAGAGGTCTGTACTTATGAG 900  
OY 901 ccaccacaggttgagacgaatcaacgaacatctgtacaatttcatgtgaagcagcagt 960  
|||||  
DB 901 CCACCCACAGTTGGCAGCTGAATTCAGACAGCTTGTGTAATTTATGTGTAACAGCAGT 960  
OY 961 tctgttgagagataaacgcgcctcacaatttcaacatcgttacctgtgaacaggaat 1020  
|||||

```

Db 961 TGCTTGGAGGGGATGAACCGCCGCTCAATTTTAATCATTTGTTACTCTGGAACACGAGAT 1020
Qy 1021 gggcaagtcctggcgagcgctgcttgaagcccgagatctgtctgcccagaagaagac 1080
Db 1021 GGGCAAGTCCTGGCGAGCGCTGCTTTGAGGCCCGGAGCTGCTGCTGCCCGCCAGGAAGAC 1080
Qy 1081 aggaagcgagatgaagatcatcagaagcagcaagcttgcagacatcagaagaagcgt 1140
Db 1081 AGGAAGCGGATGAAGATGATCAGAAAGCAGCAAGCTTTCGACAGTACAAAGAGGT 1140
Qy 1141 gatgttaagagcgccgcttgcgcagaacacacatgtaacagatgacatccatcaag 1200
Db 1141 GATGTTAGAGGCGCCCGCTTTCGTACAGACACATGATGATCCAGATGATCATCATAG 1200
Qy 1201 aaacgaagatcccaagatgtagactgttacttacttacttacttacttacttacttact 1260
Db 1201 AAACGAAGATCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1261 gaaatgctgttgaagatcaagagatcccttgaaactcaatgtaacttctctcagaacac 1320
Db 1261 GAAATGCTGTTGAAGATCAAGAGATCCCTGGAAGTATGATGATGATGATGATGATGAT 1320
Qy 1321 atgaacgttacaagcagaacagcagaacagcagaacagcagaacagcagaacagcagaac 1376
Db 1321 ATTGAACGTACAGCAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1376

RESULT 4
LOCUS AB016073 2270 bp mRNA PRI 06-FEB-1999
DEFINITION Homo sapiens mRNA for p51b, complete cds.
ACCESSION AB016073
VERSION AB016073.1 GI:3510329
KEYWORDS p51b.
SOURCE Homo sapiens
ORGANISM Homo sapiens skeletal muscle cDNA to mRNA.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2270)
AUTHORS Ikawa, S. and Osada, M.
JOURNAL Direct Submission
TITLE Submitted (10-JUL-1998) to the DBJ/EMBL/GenBank databases.
AUTHORS Shuntaro Ikawa, Institute of Development, Aging and Cancer,
DEPARTMENT Department of Cell Biology; 4-1 Seiryu-machi, Sendai, Miyagi
JOURNAL Tel:81-22-717-8484, Fax:81-22-717-8488)
REFERENCE 2 (sites)
AUTHORS Osada, M., Ohba, M., Kawahara, C., Ishioke, C., Kanamaru, R., Katoh, I.,
TITLE Ikawa, T., Nishimura, Y., Nakagawara, A., Obinata, M. and Ikawa, S.
JOURNAL Cloning and functional analysis of human p51, which structurally
MEDLINE and functionally resembles p53
FEATURES
SOURCE 98324755
location/Qualifiers
1. 2270
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3q28"
/tissue-type="skeletal muscle"
145..2070
/codon_start=1
/product="p51b"
/protein_id="BAA32593.1"
/db_xref="GI:3510330"
/translation="MSOSTQTNFSLSPVQHIWDLFQDIPGVLPIDLNLFVDPSED
GATKIKISMDICIMQSDSLSDPMPQYTMGLINSMDQIQNGSSSTSPYNTDHAQ
NVAAPSPAPSSFTALSPSPALPSPWTDYGPSPSPVQSSSTAKSATWYSTEIK
KLYCQIAKTCPIQIKVTPPGQAVIRAMVYKKAHEVTVKRCNHNELSRFNGO
IAPPSHLIRVGNASHQYVEDPTGRSVVLPPEPOVGEFTTIVINMPCNSCVGG
MNRPLILVITLETROGVLCGRCPFARICACGPRKDESDIRGOQVSDSTKNDG
TKRFRONTGIOMTSTIKRSPDDELLIYPVGRETYEMLLIKESLEIMQTLDPHT
ILEYRQOQOQHHLQKOTSIQSPSSITGNSPPLKNMNMNKLPSVQLINPQRNA

```

```

Query Match 48.9%; Score 1376; DB 85; Length 2270;
Best local similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
BASE COUNT 595 a 676 c 501 g 498 t
ORIGIN
LPTTIPDGMGANIPMAGTHMPAGDMNGLSPTQALPPRLSPSTSHCTPPPPPTDC
SLVGFARLSCSSCLDYFTTQGLITTYIYIEHRSMDLASKLTPQFRHAIWKGLDHR
OLHERSSPSHLIRTPSSASIVSVSSSEGRVIDAVFLLQRIISPPRDEWDFNF
DMDARNKQQRKEGE"
1
tcgttgaatcaaaagacagttgaagaaatgaatttgaactcaggttgcacacct 60
1
tcgttgaatcaaaagacagttgaagaaatgaatttgaactcaggttgcacacct 60
Qy 1
tcgttgaatcaaaagacagttgaagaaatgaatttgaactcaggttgcacacct 60
Db 1
tcgttgaatcaaaagacagttgaagaaatgaatttgaactcaggttgcacacct 60
Qy 61
acagatcagccttgcagccttcaatcagcagcttgcagaaacccagctcattctctg 120
Db 61
acagatcagccttgcagccttcaatcagcagcttgcagaaacccagctcattctctg 120
Qy 121
aagaagatlatcagatcccaatgctccagagacacagacagaaatgaattctcagt 180
Db 121
aagaagatlatcagatcccaatgctccagagacacagacagaaatgaattctcagt 180
Qy 181
caagaggtttccagcagatctggaatttctggaacagcctatattcagtcagccc 240
Db 181
caagaggtttccagcagatctggaatttctggaacagcctatattcagtcagccc 240
Qy 241
atgacttgaacttgttgaagacacatcagaagaatgttgtagaagaagaatgtgagatc 300
Db 241
atgacttgaacttgttgaagacacatcagaagaatgttgtagaagaagaatgtgagatc 300
Qy 301
agcatgagctgtatccgcagatcgaagagctcgagccttgagaccccatgtgccaagtac 360
Db 301
agcatgagctgtatccgcagatcgaagagctcgagccttgagaccccatgtgccaagtac 360
Qy 361
acgaacccgagcctcctgaagacagatgagacagagattgaagaagcgtctctcagacc 420
Db 361
acgaacccgagcctcctgaagacagatgagacagagattgaagaagcgtctctcagacc 420
Qy 421
agtcctataaacacagacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
Db 421
agtcctataaacacagacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
Qy 481
cccgagcctcagccttgcagccttctcctcagacagcagcagcagcagcagcagcagcagc 540
Db 481
cccgagcctcagccttgcagccttctcctcagacagcagcagcagcagcagcagcagcagc 540
Qy 541
ccagagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
Db 541
ccagagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
Qy 601
tgagcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660
Db 601
tgagcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660
Qy 661
cagatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720
Db 661
cagatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720
Qy 721
aaaaagcctgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
Db 721
aaaaagcctgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
Qy 781
gaatcaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 840
Db 781
gaatcaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 840
Qy 841
catgcccagctatgtagaagatcccatcagcagcagcagcagcagcagcagcagcagcagc 900
Db 841
catgcccagctatgtagaagatcccatcagcagcagcagcagcagcagcagcagcagcagc 900
Qy 901
ccaccccgagcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960

```

|||||  
Db 901 CCACCCAGGTTGGACAGCAATTCACGACAGCTTTGTACAAATTTTCATGTGTAACAGCAGT 960  
Oy 961 tgtgttggaaggaatgaacgcgcgtcccaatttaattcatctgttactcttgaaacaggaat 1020  
Db 961 TGTGTGGAGGAGATGACACCGCCGTCACATTTTATCATTTACTCTGTGGAACCCAGAGAT 1020  
Oy 1021 gggcaagtccttggccgagcgtctgttltgaggcccgagatctgtctgtcccgaaagagac 1080  
Db 1021 GGGCAAGTCTTGGGCCGACGCTGCTTGTAGGCCCGGATCTGTGCTGGCCAGGAAGAGAC 1080  
Oy 1081 aggaagcgaggttgaaagatagcatcaagaagcagcaagtttcggacagttacaagaagcgt 1140  
Db 1081 AGGAAGCGGATGAAGATGAGATCAGAAAGCAGCAAGTTTGGAGAGTACAAAGAACGCT 1140  
Oy 1141 gatgtacgaagcgccgcttcgtctgaagacacacatgtgtatccagatpacatccatcaag 1200  
Db 1141 GATGTACGAAGCGCCCTTTCGTCTGAGAACACACTGTGTATCCAGATACATCCATCAAG 1200  
Oy 1201 aaacgaagatcccgagatgatgaactgttatactataccagtgagggcgctggaagctat 1260  
Db 1201 AAAGGAAGATCCCGAGATGATGAATGTTATCTTACAGTGAAGGGCGCTGAGACTTAT 1260  
Oy 1261 gaaatgctgttgaagatcaaaagatccctggaactcatgacagttactcctcagacaca 1320  
Db 1261 GAAATGCTGTGGAAGATCAAGAGATCCCTGGAACATCATGATCACTTCTTCAGACACA 1320  
Oy 1321 attgaaagctacgagcaacagcaagcagcagcagccagccttactctcaaaaaa 1376  
Db 1321 ATTGAAGCTATCAGGCAACACAGCAGCAGCAGCAGCACTTACTTCAAGAAAAA 1376

RESULT 5  
AX009538 4846 bp DNA PAT 06-SEP-2000  
LOCUS AX009538  
DEFINITION Sequence 2 from Patent WO9961610.  
ACCESSION AX009538  
VERSION AX009538.1 GI:9996812  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequence.  
REFERENCE  
1 (bases 1 to 4846)  
AUTHORS Bamberger,C., Paul,D., Augustin,M. and Schmale,H.  
TITLE Tumour suppressor genes of the p53 family  
JOURNAL Patent: WO 9961610-A 2 02-DEC-1999;  
BAMBERGER CASIMIR (DE); PAUL DIETER (DE); AUGUSTIN MARTIN (DE);  
SCHMALE HARTWIG (DE); FRAUNHOFER GES FORSCHUNG (DE)  
FEATURES  
source  
1..4846  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="humane KER-"  
BASE COUNT 1372 a 1077 c 990 g 1406 t 1 others  
ORIGIN

Query Match 48.4% Score 1364; DB 9; Length 4846;  
Best Local Similarity 99.9% Pred. No. 0;  
Matches 1375; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 2 cgttgatatacaagacagttgaagaaatgaatttgaacttcacgtgtgcacacctta 61  
Db 1 CGTTGATATCAAAAGACAGTTGAGGAATGAATTTTGAACCTTCACGCTGTGCCACCTTA 60  
Oy 62 cagtagtccttcgagccttataccacagcgttctglaaaa-cacagctcatcttctgtg 120  
Db 61 CAGTACTGCTCCGACCTTACATCCAGCGTTTCGTAAGAACCCAGCTCATTTGCTTGG 120  
Oy 121 aaagaagatttcccatccacatgtccagagcaacagcaagaataaagaattcctcagt 180  
Db 121 AAAGAAAGATTATACCGATCCACATGTCACAGAGCACACAGACAAATGATTCCTCAGT 180

Oy 181 coaagagtttccagcatatctggatlttctggaacagcctatatgttcaagtcagcc 240  
Db 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAAGTTACGCC 240  
Oy 241 attgaactgaaacttgtgtagaaccatcagaagaatgtgtcgaacaacaagaattgaatt 300  
Db 241 ATTGACTTGAACCTTGTGATGAAACCATCAGAAAGATGCTGCGACAAACAAATTTGAGATT 300  
Oy 301 agcagagacttalcgcgatcagaagactcggacctgagtgagccccatgttgcccaagatc 360  
Db 301 AGCATGAGACTGTATCCGATGACAGACTCGAGACTCGAAGTGCACCCATGTGGCCACAGTAC 360  
Oy 361 aagaaccttgggctctctgaacagcaatgagaccagagatttcagaacgagcttccgtccac 420  
Db 361 ACGAAGCTGGGGCTCTGTAACAGATGAGACAGCAGATTTCAGAAAGGCTCTCTGTCAC 420  
Oy 421 agtccctataacacagaccacagcgagagaagcgttcaagcgcccttgcccttaagcaag 480  
Db 421 AGTCCCTATAACACAGACACGACGACGCGAGAAAGCGTCAAGGGGCCCTCCCTACGACAG 480  
Oy 481 cccagctccaccttcgatgctctctctccatcaaccgcccacatccctcgaacacgagctac 540  
Db 481 CCGAGCTCACCTTCGATGCTCTCTCCATCACCCGCGCATCCCTCCAAACCGACTTAC 540  
Oy 541 coagccccacagttctcgaagcgtgtcccttcagcagcagtcgagcaaccgccaagtcgacca 600  
Db 541 CCAGGCCCGCACAGTTTGGAGCTGTCCCTCCAGCAGTGGAGACCGCAATCGGCCACAC 600  
Oy 601 tggagctatcccaactgaaactgaagaactcactgccaattgcaaaagacatgcccac 660  
Db 601 TGGAGTATTCACACTGAGACTGAGAAACTTACTGCCAAATTTGCAAAAGACTGCCCCATC 660  
Oy 661 cagatcaagtgatgagcccccaactctcgaaggagctgttataccggcgaatgctgtctac 720  
Db 661 CAGATCAAGTGATGATGCCCACTCTCTCAGGAGCTGTATTCGCGCCATCCCTCTGTAC 720  
Oy 721 aaaaaactgagcaagctacaggaagtggtgaaagcggtgcccccaacatgaagctagccgt 780  
Db 721 AAAAAAGCTGAGCAACGTACGAGAGGTGTGAAGCGGTGCCCAACCAATGACTGAGCCGT 780  
Oy 781 gaattcaagaggaagaaattgcccctcctagtcatttgaattcgaatgaggggaagc 840  
Db 781 GAATTCAACGAGGAGCAAGATTGCCCTCTCTAGTCAATTGATTTCGAGTGAAGGGGAACAGC 840  
Oy 841 catgcccagttgtagaagatcccatcacaagaagagaaatgtgtgtacctatag 900  
Db 841 CATGCCAGTATGTAGAAGATCCCATCACAGGAACAGAGTGTGTACCTTATAG 900  
Oy 901 ccaaccacagttgacactgaatttcacagcagctctgtatacaatttcattgtlaacagcagt 960  
Db 901 CCACCCCAAGTTGGGACTGGAATTCACGACAGTCTTGTACATTTTCATGTGTAACAGCAGT 960  
Oy 961 tgtgttggaaggaatgaacgcgcgtcccaatttaattcaattgttactctggaacaagagat 1020  
Db 961 TGTGTGGAGGAGTAACCCGCGTCAATTTTAATCATTTTACTCTGTGAACACAGAGAT 1020  
Oy 1021 gggcaagtccttggccgagcgtctgttltgaggcccgagatctgtctgtcccgaaagagac 1080  
Db 1021 GGGCAAGTCTTGGGCCGACGCTGCTTGTAGGCCCGGATCTGTGCTGGCCAGGAAGAGAC 1080  
Oy 1081 aggaagcgaggttgaaagatagcatcaagaagcagcaagtttcggacagttacaagaagcgt 1140  
Db 1081 AGGAAGCGGATGAAGATGAGATCAGAAAGCAGCAAGTTTGGAGAGTACAAAGAACGCT 1140  
Oy 1141 gatgtacgaagcgccgcttcgtctgaagacacacatgtgtatccagatpacatccatcaag 1200  
Db 1141 GATGTACGAAGCGCCCTTTCGTCTGAGAACACACTGTGTATCCAGATACATCCATCAAG 1200  
Oy 1201 aaagaagatttcccatccacatgtccagagcaacagcaagaataaagaattcctcagt 1260  
Db 1201 AAAGAAAGATTATACCGATCCACATGTCACAGAGCACACAGACAAATGATTCCTCAGT 1260  
Oy 1261 gaaatgctgttgaagatcaaaagatccctggaactcatgacagttactcctcagacaca 1320

[illegible]

Db	61	CAACTAGCCCTGACCCCTTACATCCAGGGTTTCGTAGAAACCCACGCTATTCTCTGG	120
Qy	121	aaagaagttatattaccgataccacaatctccagaacacagaagaatatttccatg	180
Db	121	AAAGAAAGTTATTACGATTCACCACTGTCCAGACACACAGCAAAATGAAATTCCTAGT	180
Qy	181	ccagaagttlccagataatctggatttctcgaacggcctatactgtacgttcagccc	240
Db	181	CCAGAGGTTTCCAGCATATCTGGGAATTTCTCGAACAGCTTATGTACGTTCAAGCCC	240
Qy	241	attgatttaactttgtgatgtgaaccatcagaagatggtgtgaaacaaagaattgagat	300
Db	241	ATTGACTTAACCTTGTGTGATTAACCAATTCAGAAATGCTGGACAAAGATTGGAATT	300
Qy	301	agcatlgaactgtatccgcatgtgaagcctcgagaccgtgagccccatgtgtgcacagtac	360
Db	301	AGCATGAGCTGTATCCGATGCGATGAGGACACTGGAACTGATGACCCCATGTGTCCACAGTAC	360
Qy	361	acgaactctgggctccctgaacagcatgtgaaccagatctcagaacgctccctgcacac	420
Db	361	ACGAACCTTGGGCTCCTGTAAACGATGTGACCGACAGATTCAGAAAGGCTCTCTGTCCACC	420
Qy	421	agtcacctataacacagacacacgacgaagaacgctcaacggccctgtgcctatgcacag	480
Db	421	AGTCCCTATTAACACAGACACCGCGGAGAACAGGCTCAAGCGGCCCTTGCCCTACGACAG	480
Qy	481	cccaagtcacacttgatgctctctctcacaacccgcatccctcccaaacacgaatac	540
Db	481	CCCAAGTCAACTTGATGCTCTCTCTCAATCACCCGCAATCCCTTCACACCGACTAC	540
Qy	541	ccaagccgcacagtttcgaagttgccttcacagcagtcgacacgcgcaagtcgacac	600
Db	541	CCAGGCCCCACAGTTTCGAGGTGTCTTCACAGATTCGACAGTCGACACCGCAAGTGGCCACC	600
Qy	601	tggagctatctcaactcgacatgaagaactactctaccaatctgcaagaacatgcccatac	660
Db	601	TGGAGCTATTCCACTGGAAGTAAGAACTTCACTACGCCAAATTCGAAAGACATGCCCATTC	660
Qy	661	cagatcaagtgatataccacacccctcccaaggagctgttatccgacctgtgcgtctac	720
Db	661	CAGATCAAGTGATATACCCCACTCTCTAGGAGCTTTATCCGCCATGCTGTCTAC	720
Qy	721	aaaaaagctlgacacgtcaacggaagtgggtgaagcgtgtgcccaacatlgagctlgacgt	780
Db	721	AAAAAAGCTGAGCAAGTCAACGAGGTGTGTGAAGCGGTCGCCCAACCATGAGTGAACCGT	780
Qy	781	gaattcaacagggagacagattgccccctccagtcatttgatttgagtagagggaacagc	840
Db	781	GAAATTCACAGAGGGACAAATATGCCCCCTCTCTAGTCATTTGATTTGAATTAAGGGGAACAC	840
Qy	841	catgtcccaatgtatagaagatcccatcacagaagaacagatgtgtgttactctatgag	900
Db	841	CATGCCCCAGTATGTAGAAAGATCCCATCAAGAAACAGAGTGTGCTGTACTTATGAG	900
Qy	901	ccaccccaagttgtgcaatgaattacagacagctctgtacaattctcatgtgtacacagct	960
Db	901	CCACCCCAAGTTGTGCAATGAATTCACACAGCTCTTGACAAATTTCAATGTCTAACAGCAGT	960
Qy	961	tgtgttgaagatgaaacccgctgtcaatttatacttgttactcttgnaaacccagaat	1020
Db	961	TGTGTTGAGGAGTAAGAACCCGCCGTCCAAATTTTATCATTTTACTGTGAAACCAAGAGAT	1020
Qy	1021	gggcaagtcctctgggcgaagctgtcttggaaccggatcctgtgtctgtcccagaagaagac	1080
Db	1021	GGGCAAGTCCCTGGGCCACACGCTGTCTTGAAGGCCGAGTCTGTGCTTGCCACAGAGAGAC	1080
Qy	1081	aggaagggcgatagaagtagatcacagaagaacacagaattctggacaagtacaagaacggt	1140
Db	1081	AGGAAGCGCGATGAAGTAGATCAGAAACACCAAGTTTTCGACAGTACAAAGAACGCT	1140
Qy	1141	gatgttgaagcgcccgcttctgacgaacacatgttatccagatgcatcacaag	1200

Df	1141	GATGGTAGCAAGCGCCGCTTTCGTGAACAACACATGGTATCCAGATGCATCCATCANG	1200
Oy	1201	aacagagaatccccagatatgatctgttatatactaccagttagggcgctgaactat	1260
Df	1201	AAACGAGAATCCCCAGATGATGACTGTTATTACTTACCAGTGAGGGCGCGTAGACTTAT	1260
Oy	1261	gaatgcctgttgaagatcaaaagaagtccttggaactcatgacgtacctcctccagaca	1320
Df	1261	GAAAAGCGCTTGAATCAAGAGATGCCCTCGAATCATATGCACTTACCTTCCTGACACACA	1320
Oy	1321	attgaaagctcacgacaacagacagacagacagacagacagacagacagacagacagac	1376
Df	1321	ATTGAAGCTAACAGCAACAGCAACAGCAGCACAGCACTTACTTCAGAAACA	1376
RESULT	7		
LOCUS	AF075428	1347 bp	mRNA PRI 04-OCT-1998
DEFINITION	Homo sapiens TA p53 gamma mRNA, complete cds.		
ACCESSION	AF075428		
VERSION	AF075428.1	GI:3695077	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1347) Yang,A., Kagniad,M., Wang,Y., Gillett,E., Fleming,M.D., Dotsch,V., Andrews,N.C., Capcut,D. and McKeon,F. p53, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities Mol. Cell 2 (3), 305-316 (1998) 98448095 2 (bases 1 to 1347) Yang,A., Kagniad,M., Capcut,D. and McKeon,F. Direct Submission Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240 Longwood Ave, Boston, MA 02115, USA FEATURES Source Location/Qualifiers 1..1347 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3" /map="3q27-q29" 1..1347 /function="transcription factor" /note="First splice variant; related to p53 and p73" /codon_start=1 /product="TA p53 gamma" /protein_id="AAC62633.1" /db_xref="GI:3695078" /translation="MSOSTQVNEFLSPYRHOIMDFLEPQICSVQPIDLNFVDPESE GATKIEISDCKIRMOUSDLSDPMPOTTNIGLNSMDQIQONSSSTSPNTDHADN SVAPSPYAQSFTFDALSPSPAIPSTNDTPGSLFVSFEQSSATASTVYSTELK KLVCOKIKTCPIQIKVMTPPOGAVIIFAMPYKKAEHYTEVKRPNHIELREFNEGQ IAPSRLIRVEGNHAQVEDPIRGROSVLPVPPOVGTFETVLIVNFKNSSCVSGAS MKRRPLITVTLETGRDOVIGRCFAERICACPERDRKADDSDIRKOVSSTKNNGG TKREPRNTGICQMSTSIKKRSPPDELLIYPVRERREYEMLIKRESLELMQIYPTPT IETTRQOQOOOHQLHLNLHSACFRNELVEPRRETROSDFVFRRHKPPNRSYVP"		
CDS			
BASE COUNT	374 a	381 c	317 g 275 t
ORIGIN			
Query Match	47.8%;	Score 1347;	DB 88; Length 1347;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1347;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Oy	145	atgtccagagacacacaaatgaatcccacatccaagagtttccagcatactcg	204
Df	1	ATGTCCAGAGACACACAAATGAATTCCTCATCCAGAGGTTTTCCAGCATATCTGG	60
Oy	205	gatttcctggaacagcctatatgttcagltccagccataggtaactgttgatgaa	264

D	b	61	GATTTTCGAAACAGCCTAATATGTTTCAGTTCAGCCCAATTGACTTGAACTTTGTGATGATA	120
Q	y	265	ccatcaagaaga tgg tgc gaa caa aaga att gga att l aaga tga cga tgc t a tcc gca tgc ag	324
D	b	121	CCATCAGAAAGATGGTGGCACAACAAAGATTGAAATTAGCATGAGCTGTAATCCGCATGCAG	180
Q	y	325	gactcgagcccttgag tga ccc cca tgc tgc gca cag taca gaa acc tgg ggc ttc tga cag c	384
D	b	181	GACTCGAGACTGAGTGAACCCATGTGGCCACAGTACACGAACTGGGGCTCTGTAACAGC	240
Q	y	385	atggaaccaaga att caga aag cgt cct tgc tca cca g tcc ctata taca caga cca g c g	444
D	b	241	ATGGACACGACGAATTCAGAAAGGGTCTCTCTCCACCAAGTCCATTATMACAACACCAACGCG	300
Q	y	445	cagaacag cgt cca ag ggc cct tgc ccc t a g ca c a g c c c a g c t c c a c c t t g a t c t c	504
D	b	301	CAGAACACCGTACAGGGGCGCTGACCTTAGCACAAGCCAGCTCCACCTTGATGATCTCTC	360
Q	y	505	tctccatcaaccgcgc at ccc cct ccca aac cga attaca gaa ccc gca cag att tgc ag t g	564
D	b	361	TCTCATCACCCTGGCCATTCCTCCCAACACGAGCTACCCAGGGCCGACAGTTTCAGCGTG	420
Q	y	565	tcc ttc cag cag tgc g a c a c c g c a a g tgc g c a c c t t g a c g t a t t c a c t g a a g	624
D	b	421	TCTCTTCACGACGAGTGGAGACCGCCAAATCGGCCACCTGGACGTAATTCCTGAACCTGAGAG	480
Q	y	625	aaactctctccaa att tga a a g a g a c tgc ccc atcc gata c a a g t g a t g c c c a c c t	684
D	b	481	AAACTCTACTCCCAATTTGGCAAAACATGCCCCATCCAGATCAAGGTATGACCCCACT	540
Q	y	685	cctcagggagctgt t a t c c g c g c a t c c t g c t a c a a a a a g c t b a g a c a g t c a c g a g	744
D	b	541	CCTCAGGGAGCTGTATTATCCGGCCATCCCTGTCTACAAAAAAGCTAGCAGCTCACGGAG	600
Q	y	745	gtgtgtgaagcgg tgc ccc caa cca t b a g c t g a g c g t g a a t t c a a c g a g g a c a g a t t g c c	804
D	b	601	GTGGTGAAGCCGCTCCCAACCAATGAGCTGAGCGGTGAATTCAACGACGGACAGATTTGCC	660
Q	y	805	cctcctag tca tt g t t g t a g t a g a g g a a a g c a a t g c c a g a t g t a g a a a t a t c c	864
D	b	661	CCTCCTACTCATTTTGATTTCAGTAGAGGGGAACAGCCATGCCCCAGATATGAAAGATGCC	720
Q	y	865	atcacaagaaga c a g a g t g t g c t g t g a c c t t a g a c c a c c c a a g t t b g c a t g a a t t c	924
D	b	721	ATCACAGGAACACAGAGTGTCTGTACTTATGACCAACCCAGSTTGGCACTGAATTC	780
Q	y	925	acgacag t c t g t a c a a t t t c a t g t g a a c a g c a g t t g t t g a g g a t g a a c c g c g t	984
D	b	781	ACGACAGCTTGTAACAATTTTCATGTGTAAACAGAGTGTGTGAGGATGAACCGCCGT	840
Q	y	985	ccaatttaacatcat t g t t a c t c t g g a a c c a g a g a t g g g c a a g t c c t t g g c c g a a g c t g c	1044
D	b	841	CCAATTTTAAATCATTTGTACTCTGGAACACAGAGATGGCAATCTCTGGCGGACGATGC	900
Q	y	1045	tttgagcccgag t c t g c t t g c c c a g a a g a c a g a a g c g g a t g a a t a t a g a t c	1104
D	b	901	TTTGAGGCCCGGATCTGTGCTGCGCCACGAGAAAGACAGAGAAGCGGATGAATATAGCATC	960
Q	y	1105	agaaagcagcaag t t c g a c a g t a c a a a g a c g t g a t g t g t a g a a g c g c c g t t g c t	1164
D	b	961	AGAAAGCGAGAGTTTGGACAGTACAAAGAAAGGGTGAATGATACGAAGCGCCCTTTTGGT	1020
Q	y	1165	cagaacacac t g t t a t c c g a a t g a c a t c a a t a a a a a c g a a g a t c c c c a a t g a t a a	1224
D	b	1021	CAGAACACACATGGTATTCAGATGACATTCATTAAGAAACGAAGATCCCCACATATATGAA	1080
Q	y	1225	ctgtataactta c a g t g a a g g g c g t g a a c t t a g a a t c t g t t g a a t c a a a g a g	1284
D	b	1081	CTGTATTACTTACACAGTGAAGGGCGGTGAGACACTTATGAATAATCCTGTGTGAAGATCAACAG	1140
Q	y	1285	tccctgaaactca t g c a g t a c t t c c t c a g c a c a a a t t g a a a c g t a c a g c a a c a g a a	1344
D	b	1141	TCCCGGAACATCATGACGTAATCTTCCACCAACACATTTGAACGTAACGGCAACAGCA	1200



QY	1345	cgagcagcagcaccagcacttaacttaagaacatctcccttcagcctgtcttcgaatgag	1404
Db	1201	CGAGCAGCACACACACACTTACTTACGAAACATCTCTTTCAGCCCTGCTTCAGGAATGAG	1260
QY	1405	ctgtgtgagcccccgagagaagaactccaacaacatctgacgtctctcttaagatcccaag	1464
Db	1261	CTGTGTGAGCCCCCGAGAGAAACTCCAAACATCTGACGCTTCTTTCAGACATTCCAAAG	1320
QY	1465	cccccaaccgatacgtgtaccatga	1491
Db	1321	CCCCCAACCGATCAGTGTATCCCATAG	1347
RESULT	8		
LOCUS	AF075432	1551 bp	mRNA
DEFINITION	Homo sapiens	TA p63	beta mRNA, complete cds.
VERSION	AF075432.1	GI:3695085	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 1551)		
TITLE	Yang, A., Kagnad, M., Wang, Y., Gillette, E., Fleming, M. D., Dotsch, V., Andrews, N. C., Caput, D. and McKeon, F.		
JOURNAL	p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities		
MEDLINE	Mol. Cell 2 (3), 305-316 (1998)		
REFERENCE	98448095		
AUTHORS	2 (bases 1 to 1551)		
TITLE	Yang, A., Kagnad, M., Caput, D. and McKeon, F.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240		
AUTHORS	Longwood Ave, Boston, MA 02115, USA		
FEATURES	Location/Qualifiers		
source	1..1551		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/chromosome="3"		
	/map="3q27-q29"		
	1..1551		
	/function="transcription factor"		
	/note="fifth splice variant; related to p53 and p73"		
	/codon_start=1		
	/product="TA p63 beta"		
	/protein_id="AAC62637.1"		
	/db_xref="GI:3695086"		
	/translation="MSSTQYNEFLSPFQHIWDFLEPQICSVOPIDLNVPDPESEEGATWPKIEISMDICIMODSLSDPMMPQVOTNLGILNSMDQOIONSSSPVNTPHADON		
	SVNTPSPYAPDSSTPFEDLSBPSPALPNTDYGPRHSFVDSFOOSTAKSATVITYTELK		
	KLYCOIATCPDIQIKVMTPEPQGAIVIRMPYKKAHEVTEVKRCPNELSERNEG		
	IAPSHLILVLETRDGOVLGRFCFPAICGPGDRKADSDSIRKQVSDSTNCGD		
	TKRFRONTNHIQMTSIKRRSPDELLYLIVRREYEMLKIKESLIMQYLPQHT		
	IEYRQOOOQOHHLQKOTSIQSSPSYGNSSPLNNKNSNNKIKPSVQLINPOORNA		
	LTPTPTDGMKANIPMGTHIPMAGDMNGLSFTQALPPLPLSPSTSHCTPPPTPTD		
	STIVIMQY"		
BASE COUNT	425 a	466 c	350 g
ORIGIN			310 t
Query Match	43.8%	Score 1232:	DB 88: Length 1551;
Best Local Similarity	100.0%	Prod. No. 1.6e-289;	
Matches 1232: Conservative	0;	Mismatches	0;
		Indels	0;
		Gaps	0;
QY	145	atgtccacgagcaccacaacaatgaatccctcagctccagaagtttccagcatactcg	204
Db	1	ATGTCCACGAGCAGACAGCAAAATGAATTCCTCAGATCCAGAGGTTTCCAGCATATCTGG	60
QY	205	gatttctcgaacagcctataatgtcagctcgaagccatgacttgaaacttctgtgatgaa	264

Db	61	GATTTTTCGGAAACGCTATATGTTCAGTTTCAGCCCATTTGACTTGAACCTTTGTGCATGAA	120
Qy	265	ccatcaagaagaatggctgcgaacaaagaattgagattagaatgagatgctatccgcatacgag	324
Db	121	CCATCAGAAGATGTGGCGACAAACAAAGATTGAGATTAGCATGAGTATGTATCCGACATGCG	180
Qy	325	gactcggagccctcgagttgagcccaatgctgagcacaagtacaagaacctggaggtccttgaacgc	384
Db	181	GACTCTGGACCTGAGTGNACCCCATTTGGCCACAGTATACGAACAACTGGGGGCTCTTGAACAG	240
Qy	385	atgagcaccgaagattcgaagaagctctcgtgtccacgaatccctataaacaagacaagcg	444
Db	241	ATGGACACGACGAGATTTCAGAAAGGCTCCTGTCACACGATCCTATATACACAGACACGCG	300
Qy	445	cagaacagcgtcaacgycgcacctcgccctacgcacaagcccagacttcaaccttcatgctctc	504
Db	301	CAGAACACGCTACAGGGCGCCCTCGCTCCCTTAGCAGACGCGCAGCTCCACCTTTCATGCTGTC	360
Qy	505	tctcatcaaccgcgaatccctctccaacaaccgaattaccagagcccgacaagtttcgaagt	564
Db	361	TCTTCATATACCCGGCATTCCTCCCTCCMACACCGATACCCAGGCGCCGACAGTTTTCACAGTG	420
Qy	565	tccctcgaagctcgaagcaccgcgaagtctggcacccttgagacttaccattcaacttgaag	624
Db	421	TCTCTTCAGCAGTGGAGCACCGCCAAATCGGCCACCTGGACGTAATTCCTCACTAAGCTGAG	480
Qy	625	aaactctactgcgaatlgcaaaagacatggcccatcgaatcaagatcaagtgaatgacccacct	684
Db	481	AAACTCTACTGSCAAATTTGCAAAACATATGCCCATCCATCCAGATCAAGTAGATGACCCACCT	540
Qy	685	cctcagggagctgtatccgcgcacaatgctgtctctcaaaaaagcttgaagcagtcagag	744
Db	541	CCTCAGGAGCTGTTATTCGGGCGCATCCCTGTACAAAAAATCTGAGCAGCTTCACGGAG	600
Qy	745	gtggtgaagcgggtgccccacaactgaagcttgaagcctggaattcaagaaaggacaagttgac	804
Db	601	GTGGTGAAGCGGTCGCCCAACCAATGAGCTGAGCGGTGAATTCACACGAGGACAGATATGCC	660
Qy	805	ccctctatcatcttggatctcgaatgaaggaaggaacagcaatgcccagatgtagaagaatccc	864
Db	661	CCTCTTACTCATTTTGATTTCAGATGAGAGGGAACAGCATATCCACAGTATGTAGAACATCCC	720
Qy	865	atcacaggaagacagagtgctgtgtactaactatgagccaaccacgaattgycacatgaatlc	924
Db	721	ATCACAGGAACACAGAGTGTGCTGTACTTATGAGCACACCCAGGTGGACTGAATTC	780
Qy	925	acgaagctctgtataatlttcatgtgtgtaaaagcaagtgtgtgttggagagatgaacccgcgt	984
Db	781	ACGACAGCTGTGTCAAATTCATGTATGTAAACAGAGTTGTTGGAGAGTGAACCGCGCT	840
Qy	985	coaatcttaatcatctgttactctcgtgaacacagagatgggcgaagctccctggccgaagctgc	1044
Db	841	CCAAATTTTAATCATTTGTTACTCTGTGGAACACAGAGATGGCGCAAGTCTCTGGGCGCAGCTGC	900
Qy	1045	tttgaagcccgagatctgtgctcttgcccaagaagaagacaaggaagtcggaatgaagatagcatc	1104
Db	901	TTTGAGCGCCGAGTCTGTGCTTGGCCCGAAGAGACAGGAAGGCGGATGAAGATGACATC	960
Qy	1105	agaaagcagcaagttctcggaacagtacaagaacggtgtgattgtaagaagcgcgcttgcgt	1164
Db	961	AGAAAGCGACGAAATTTTGGAGACAGTACAAACAAAGGTGATGACGAAGCGCCCTTTTGGT	1020
Qy	1165	cagaacacaaatgttatccagaatgacatccaataaagaacgaagaatcccccaatgaatga	1224
Db	1021	CAGAACACACATGTGTATTCAGATGACATTCATTAAGAAACGAAGATCCCCACATATATGA	1080
Qy	1225	ctgtataacttaacagatgagagggcgctggaacttatagaatctgttgaagatcaagaag	1284
Db	1081	CTGTATATCTTACAGAGTGAAGGGCGGTGAGAACCTTATGAATCTGTTGAAGATCAAAAG	1140
Qy	1285	tcacctggaactcatgacgtaacctctcagcacacaaatgaaacgtacaagcaacagcaa	1344



Db	1141	TCCCTGGAACTATCATCTAGTACCTTCCTCAGCACCAATTTGAAAGCTACAGGCACACGCAA	1200
Oy	1345	cagcagcacgacccagctacttacttcagaaca	1376
Db	1201	CAGCAGACGACACCGACTTACTTGAGAACA	1232
RESULT	9		
LOCUS	AF075430		PRI
DEFINITION	Homo sapiens TA p53 alpha mRNA, complete cds.		04-OCT-1998
ACCESSION	AF075430		
VERSION	AF075430.1	GI:3695081	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 1926)		
AUTHORS	Yang,A., Kagnad,M., Wang,Y., Gillett,E., Fleming,M.D., Dotisch,V., Andrews,N.C., Caput,D. and McKeon,F.		
TITLE	p53, a p53 homolog at 3q27-q29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities		
JOURNAL	Mol. Cell 2 (3), 305-316 (1996)		
MEDLINE	98448095		
AUTHORS	2 (bases 1 to 1926)		
TITLE	Yang,A., Kagnad,M., Caput,D. and McKeon,F.		
JOURNAL	Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240 Longwood Ave, Boston, MA 02115, USA		
FEATURES	Location/Qualifiers		
source	1..1926		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/chromosome="3"		
	/map="3q27-q29"		
	1..1926		
CDS	/function="transcription factor"		
	/note="third splice variant; related to p53 and p73"		
	/codon_start=1		
	/product="TA p53 alpha"		
	/protein_id="AAC62635.1"		
	/db_xref="GI:3695082"		
	/translation="MSQSTQTEFLSPVEFQHIMDFLEOPICSVOPIDLNFDEPSESDGATKKEISMCSIRMDQLSDPMMPQYTNGLINSMDQIQONSSSTSPDYNHAONSVTPSPYAOPSFFEDLASPSPAITPDVGPSPSPVSFOOSAKSATMYTSTEKLKYQIAKTCGTQIKVMTPPGQAVITAMPYIKAEHYEYVKRCNHELSRENECIAPSHILRVBGNSHAQVEDPTIGRQSLVPYPPOVGTEFTVLNFMCNSSCVGGMNRPLIIVTLERDQVLRFCFEARICAPGRDKADEDSIRKOQVSDSTNGGSGTKRPFRONTINGIOMTSIKRRSPDELIYLPVREREYEMLKIKESLEIMQYLPORTETRYROOQOOHOHLIKOTSIOSPSSYGNSPLNMKNMSMKLPSYSOLINPOORNALETPTIDGMGANIPMGTHHPMAGMDNGNLSPQALPLPISMSTSCTPPPYPTPCSYSEFVARLCSSLDYFTTOGLTYITYIEHSMDLASLIKIPQRFRAHIYKGLIDRRQLHFESSHILRTPPSSASTVSVSSSETRGERVIDAVFTLQRITISPPRDWMDFNFMDDMRKKMQDIRKEGE"		
BASE COUNT	509 a 574 c 444 g 399 t		
ORIGIN			
Query Match	43.8%; Score 1232; DB 88; Length 1926;		
Best Local Similarity	100.0%; Pred. No. 1.ee-289;		
Matches 1232; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Oy	145	atgtcccgaggagcaccaaacaaatgaattcttcagtccaagaggtttccagaatatctgg	204
Db	1	ATGTCCCCAGACGACACCAACAATAATTCCCTCACTCCAGAGGTTTTCCACCATATTCGG	60
Oy	205	gatttcgcgaacaaccatattgttcagttcaagccattgaacttgatgatga	264
Db	61	GATTTTCTGGGAACACCCTATATGTTCACTTCAGGCCATTGACTTAACTTTGTGGATGAA	120
Oy	265	ccatcagaagaatgtgtgcacaacaagaattgagattgacatgacctgcacatgcatg	324

Db	121	CCATCAGAGATG	GTGGCAGCAAAACAGATTGAGATTAGCATGAGACTGATTCCGACATGCAG	180	
Qy	325	gactcgagccctgag	tgaaccccaatgtgccaag	tacacgaacctggggtccctgaacagc	384
Db	181	GACTCGAACCTG	GAATGACCCCATGTGTGGCCACAGT	AACGNAACCTGGGGCTCTTGAAACAGC	240
Qy	385	atggaacgacagat	tccagaaagctccctg	tccacagctccctataacacagacagcgcg	444
Db	241	ATMGACACGACG	ATTTCAGAAAGGGCTCTCTGTCACAGATCCCTATTAAACACAGACACGCG	300	
Qy	445	cagaaacgagtc	caagggccctcgccct	taagacaagcccaagctccaaccttgatgctc	504
Db	301	CAGAACACAGCT	GCACGGGCGCCCTGCGCTTACGACACACCCAGCTCCACCTTCGATGCTTTC	360	
Qy	505	tcctcatcaaccgc	catccctccaacacgnaataccagagccgcgaagtttgaagtg	564	
Db	361	TCTCATATACCC	GGCCATCCCTCCCAACCCGACTTACCAGGCCCCACAGTTTGACGTG	420	
Qy	565	tccttcacgacag	tcgagcacgcgaagtcg	ggccacttgaacglattcacatgaactgaag	624
Db	421	TCTCTTCAGCAG	TGAGACACGGCAATGCGGACCTGGACGATTCACCTGAACTGAAG	480	
Qy	625	aaactctactgc	caaatatgcaagaacatgc	cccaatccagataaaggtgatgccccacct	684
Db	481	AAACCTACTCTG	CCAAATTTGGAAAGACATGCCCCATCAATCAATCAAGTGATGACCCCACT	540	
Qy	685	cctcaaggagatgt	ctatccgcgcacatgcctctgt	tacaaaaaagcttgaagaagtcacagag	744
Db	541	CCTCAGGAGCTG	TGTTATCCCGGCATGCTCTTACAAAAGCTTGAGCACCTCACGGAG	600	
Qy	745	gttggtgaagcgt	gtgcccccaacatagagcttga	gcgtgaatcaacagaggaacaagattgccc	804
Db	601	GTGGTGAAGCG	TGTCGCCCAACATGAGCTGACCGTGAAATTCACAGAGGACAGATTGCG	660	
Qy	805	cctcctatgcat	ttgtatgtagaggggaacacgaatgc	cccgatgtagaagaatccc	864
Db	661	CCTCTACTCTAT	TTTTGATTTCAGTAGAGGGGAAACGCCATGCCCCAGTAGTAGAATAATCCC	720	
Qy	865	atcaacaggaaga	cagagtgctgctcgtaacctat	gagcaaccccaagtttgacatgaatc	924
Db	721	ATCACAGGAAG	ACAGATGTGTGTAACCTTATGAGCACCCAGTTGTGACTAATTCC	780	
Qy	925	acgacagctctga	caaatcttaactatgt	gtaaaagcagttgttgaagggaatgaacccgcgt	984
Db	781	ACGACAGCTGT	GTACAAFTTCATGTGTAAACAGAGTTGTGTGAGAGGATGAACCGCGT	840	
Qy	985	ccaatttcaatc	atgttactcttggaaacacagat	tgggcaagtccttgggcccgaagctgc	1044
Db	841	CCAATTTTAACT	TTGTTACTCTGTGAAACACAGAGATGGGCAAGTCTCTGGCGCAGAGCTGC	900	
Qy	1045	tttgaagcccgag	atcctgtgctctgcccaggaagaagaaagcggaatgaagaatgc	1104	
Db	901	TTTGAAGCCCG	AGATCTGTGCTTGCCCGAGAGAGACAGAGAGCGGATGAAATGACATC	960	
Qy	1105	agaaagcagcaag	ttcttggacaatlaacaaagaaagtgat	tgatlaagaaagcccgcttctgt	1164
Db	961	AGAAAGCAGCA	AGTTTGGAGACAGTAAAGAAAGAGGTGATGTATCGAAGCGCCGTTTGT	1020	
Qy	1165	cagaacacacat	gtgtatccagatgaacatc	atcaagaagaagaatccccagatgaatga	1224
Db	1021	CAGAAACACAT	TGTGTATTCAGATGACATCCATCAAAAGAAAGATCCCAAGATGATGAA	1080	
Qy	1225	ctgttataactac	agatgaagggcggttgaagactatga	aagtctgttgaagaataaagaag	1284
Db	1081	CTGTTATATCT	TACCAAGTAGGGGCGGTGAGACTTATGAATACTGTGTAAGTCAAAAG	1140	
Qy	1285	tcacctgaactac	gagatlaaccttccctcagacacacat	tgaaagctacagggaaacagaa	1344
Db	1141	TCCCTGGAAC	TACGAGTAGTACCTTCTTCAGACACACATTTGAANCGTACAGCAACAGAA	1200	
Qy	1345	cagcagcagcag	cagcactacttccagaaaca	1376	
Db	1201	CAGCAGCAGC	ACACGACTTACTTGAGAAACA	1232	

RESULT 10  
AF075434 1452 bp mRNA ROD 04-OCT-1998  
LOCUS Mus musculus tr\**p53* gamma mRNA, complete cds.  
DEFINITION AF075434  
ACCESSION AF075434.1 GI:3695089  
VERSION  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Yang, A., Kaghad, M., Wang, Y., Gillett, E., Fleming, M.D., Dotsch, V., Andrews, N.C., Caput, D. and McKeon, F.  
TITLE *p53*, a *p53* homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities  
JOURNAL Mol. Cell 2 (3), 305-316 (1998)  
MEDLINE 98448095  
REFERENCE 2 (bases 1 to 1452)  
AUTHORS Yang, A., Kaghad, M., Caput, D. and McKeon, F.  
TITLE Direct Submission  
JOURNAL Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240 Longwood Ave, Boston, MA 02115, USA  
FEATURES  
source Location/Qualifiers  
1.1452  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/chromosome="16"  
1.1452  
/function="transcription factor"  
/note="first splice variant; related to *p53* and *p73*"  
/codon\_start=1  
/product="tr\**p53* gamma"  
/protein\_id="AAC62639.1"  
/db\_xref="GI:3695090"  
/translation="MNEFTSKATLLQYCPDPYIOTFIETPAHFSKESYRSANSOST  
OTSEPLSEVFOHIDLEOPICAVPTIELNFEPSNGATNKIEISMDIRMODSD  
LSDPMQYTNGLNLSMDQOIONGSSSTSPYNDHAQNSVPAQSPASPTDALS  
PSPALPNTDYPGHSPFVDSFOGSSSTAKSATWYSTETKRIKXOATATCPQIOTVMP  
PPQAGAVIRAMPYVYKAEHTEVYRCRPHNELSREPNBQIAPPSHLIRBEGNSHAQYV  
EDPIRGROSLVYPERPOVGYEFTVTLNEMKNSCYGGMRRPILIIIVLEKDGQV  
IGRRCFEARKTACGPRDRKADSDIRKQVSDSAKNGDAFQONHGIOMSIKKRRSP  
DELLYLTPVRGRTYEMLLKIKESLELMQYLPQHTIETRYROOQOQOHLLQKHLISA  
CFRDELVYPRREAPFQSDVFFRHSPNPMHSYVP"  
BASE COUNT 394 a 427 c 341 g 290 t  
ORIGIN  
Query Match 43.3%; Score 1219.6; DB 94; Length 1452;  
Best Local Similarity 90.6%; Pred. No. 1.7e-286;  
Matches 1327; Conservative 0; Mismatches 124; Indels 13; Gaps 2;  
29 atgaatttgaactcagcagtggtccacccctacagctactgcccagacccttaactcaag 88  
Db 1 ATGAATTTTGAACATTCACGCTGTCACCTACAGTACTGCCCCGACCTTACATCCAG 60  
Qy 89 cgcttcgtagaaga-cccgagctcaattctctcttggaaagaagttaattacagatccaacatg 147  
Db 61 CgTTCATAGAAACCCCGAGCTCATTTCTCGTGAAGAAAGAAAGTTATTATAGATCTGCCATG 120  
Qy 148 tccagagcacacagacagaatgaattctctcagtcagcagaggtttccagacatatcggat 207  
Db 121 TCGCAGACACCCAGACAGAGGAGTCTCTCAGGCCAGAGGCTCTTCCACCATATCTGGGAT 180  
Qy 208 ttctctgacacagcctatactgttcaagctcagcccatctgacgtgaacttggtgatgaacca 267  
Db 181 TTTCTGGAACAGCCCTATATGCTCACTACAGCCCATCGAGTTGAACCTTTGTGATGAACCT 240  
Qy 268 tcagaagatggtgcgacaacaagaattagattagcagtgagctglatccgcatgcagagac 327  
Db 241 TCCGAAATAGTGTGCAACAAACAGATTGAGATTGAGCATGATGTATCCGATCCAGAC 300

Qy 328 tcggaactgaatgaccccaatgtgcccacagatcacagaaacttgaggctctcctaacaagatg 387  
Db 301 TCAGACTCAGTACCCCTATGTCGACACAGTACAGAACTGGGGCTCTGAAACAGCATG 360  
Qy 388 gaccagcagaattcagaagaagcgtcctcgtccacagatccctataacacagaacacagcag 447  
Db 361 GACACGACATTCAGAAAGGCTCTGTCACACACCCCTTACAAACAGACACACACAG 420  
Qy 448 aacagcgtcagcgcgcctcgcctcagcagacagccagcagctccactgaatgctctct 507  
Db 421 AATGAGTGAGGCGCCCTCGGCCCTATGACAGACCCACTTCCACTTTGATGCTCTCT 480  
Qy 508 ccataccgcagcctccctccacaacacagacacagcagcagccgcagcagcttcagcgtctcc 567  
Db 481 CCATCCCTCGCATTCCTCTCCAAACAGATTACCGGGCCACACAGCTTGATGTGTC 540  
Qy 568 ttccagcagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 627  
Db 541 TTCCAGCAGTCAAGCAGCTGCCAAGTCAGCACTGAGAGTTCACCGAAGTGAAGAG 600  
Qy 628 ctctactgccaatgtcaagaacatgcccacatccagatcaagtgatgaacccactcc 687  
Db 601 CTGTACTGCGAGATTGCGAAGCATGCCCATCCAGATCAAGTGATGACCCCA 660  
Qy 688 cagggaagctgttattcgcgcagcagcagcagcagcagcagcagcagcagcagcagcagc 747  
Db 661 CAGGGCGTGTATCCGTCGATGCTCTCTTCAAGAAAGCTGAGCATGTGCACGAGT 720  
Qy 748 gtgaagcgtgcccacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 807  
Db 721 GTGAAGCATGCCCTTACCATGAGCTGAGCCCTGATTAATGAGGAGATGAGCCCT 780  
Qy 808 cctagcaattgattcaggaatgaggaagcagcagcagcagcagcagcagcagcagcagcagc 867  
Db 781 CCGAGTATCTGATTCGATGAGTGAAGAGCAAGCATGCCAGTATGTAAGAAATCTCATC 840  
Qy 868 acaagaagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 927  
Db 841 ACGGAAGGCGAGAGCTGCTGCTCTTATGACACACAGTGGCTGACTGAAATTCACA 900  
Qy 928 acaactctgtacaattcagatgtgtaacagcagcagcagcagcagcagcagcagcagcagc 987  
Db 901 ACACTCCGTGATTCATGATGTGTAACAGCAGCTGCTGAGAGATGAACAGACGCTCA 960  
Qy 988 atttaactcattgtactcctctggaacacagagatgaggcagcagcagcagcagcagcagc 1047  
Db 961 ATTTAATCATCTGATCTGTAAGAACAGATGGCAAGTCTGGGCGGACGCTGTT 1020  
Qy 1048 gaggcccgagctcgtgctgcccaggaagagacaggaagcagcagcagcagcagcagcagc 1107  
Db 1021 GAGGCCCGGATCTGTCTGCTCCCAAGAAAGACCGGAGGAGAAAGTGAAGACACATTCAGA 1080  
Qy 1108 aagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1167  
Db 1081 AAGCAGCAAGTATCGACACGCAAGAAAGAGCGGAGT-----CTTCCGCTGAG 1128  
Qy 1168 aacacacatggtatccagatgacatcatcaagaagaagatcccccagatgattgaactg 1227  
Db 1129 AATACACAGGAATCCAGATGACTTCCATTAAGAAAGGAGATCCCAATGATGAGCTG 1188  
Qy 1228 ttaactactcaagtgagggcgctgagacttaagaaatgctgttgagaatccaagatcc 1287  
Db 1189 CTGACTTACACAGTGAAGAGTCTGAGAGCTAGAGATGTGCTGTAAGATCAAAAGGTGA 1248  
Qy 1288 ctggaatctatgtgaatcctctcagcagcacaatgtgaacgtacagcagaacagacag 1347  
Db 1249 CTGAGCTCATGAGTACCTCCCTCAGCACACGATGAAACGTAACGACAGCAGCAG 1308  
Qy 1348 cagcagacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1407  
Db 1309 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1368

QY 1408 gtgagcccccagagaaacccaacatctgacgtctcttagacatccaagccc 1467  
|||||  
DB 1369 GTGAGCCCCCGGGGAGAGCTCCGACACAGTGTGACGTCTTTTAGACATCCAAACCC 1428  
QY 1468 ccaaacgcagatcagtgaccatag 1491  
|||||  
DB 1429 CCAAAACCACTCGCTGACCACATAG 1452

RESULT 11  
RSET 4991 bp mRNA ROD 19-APR-2000  
LOCUS RSET Rattus norvegicus mRNA for TA2 KET alpha protein (p63 gene).  
DEFINITION Y10258.2 GI:7630116  
ACCESSION Y10258.2 GI:7630116  
VERSION p63 gene; TA2 KET alpha protein.  
KEYWORDS Norway rat.  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 4991)  
AUTHORS Schmale, H. and Bamberger, C.  
TITLE A novel protein with strong homology to the tumor suppressor p53  
JOURNAL Oncogene 15 (11), 1363-1367 (1997)  
MEDLINE 97460723  
REFERENCE 2 (bases 1 to 4991)  
AUTHORS Schmale, H.  
TITLE Direct Submission  
JOURNAL Submitted (23-DEC-1996) H. Schmale, Institut fuer Zellbiochemie und  
Klinische Neurobiologie, Universitaetskrankenhaus Eppendorf,  
Martinstrasse 52, D-20246 Hamburg, FRG  
REMARK 3 (bases 1 to 4991)  
AUTHORS Schmale, H.  
TITLE Direct Submission  
JOURNAL Submitted (18-APR-2000) H. Schmale, Institut fuer Zellbiochemie und  
Klinische Neurobiologie, Universitaetskrankenhaus Eppendorf,  
Martinstrasse 52, D-20246 Hamburg, FRG  
COMMENT On Apr 20, 2000 this sequence version replaced gi:2437846.  
FEATURES  
source Location/Qualifiers  
1..4991  
/organism="Rattus norvegicus"  
/sub\_species="Wistar"  
/db\_xref="taxon:10116"  
/tissue\_type="lingual epithelium"  
/clone\_lib="circumvallate taste papilla library"  
gene 148..4940  
/gene="p63"  
148..2190  
/gene="p63"  
/function="putative role in development"  
/codon\_start=1  
/product="TA2 KET alpha"  
/protein\_id="CAB88216.1"  
/db\_xref="GI:7630117"  
/translation="MNPETSRCAITLYCPDPYIQRITFSPHSKESYSASMSOST  
OTSEFLSEVQHIWDLFDPIICVOPIDILNFDVDEPSNGATNKIEIMDCIRMDSD  
LSDPMWQYTNGLINGMDQIQNGSSSTSPYNDHAGNSVAPSPVAPSPSTEDALS  
PSPAIPSTWDYPGHSEDFVSFOQSTASAWTYSTELKLYCQIAKCPIDIKMTP  
PPQCAVIRAMVYKKAHEVVKRCPNHELSENEGQIAPSHLIVEGNSHAYV  
EDPTGRQSVLPYEPQVGTGEFTVLVFNQNSCVGGMRRPILITVLETRGOV  
LGRCEARICACGGRKADKEDSIRKQVDSAKNGCTGRRPONTNGHGMSTIRK  
RRSPDELLIYPRGRETYEMLIKESLELMQYIPQTIETTRQOQOQOHLOKO  
TSMQSSYGNSSPPLNKMNSMKNLPSVQLINPOQRNALPTTTPPEMGANIPMG  
HMPAGDNGSLSPQALPPLSPMSTSHCTPPPYPTDCISVSLFARLGCSSCLDYFT  
TQGLTTIYQIEHYSMDLAKIPEQFRHALIMKGLDHRQLHDESSPHLLRTPEGAS  
TVSYSETREGRVIDAVRFTLRQTISSPPDENMDFNMDSRNKKQRIKEEE"  
4935..4940  
/gene="p63"  
polyA\_signal  
BASE COUNT 1362 a 1157 c 1084 g 1388 t  
ORIGIN

Query Match 41.4%; Score 1166.2; DB 95; Length 4991;  
Best Local Similarity 91.0%; Pred. No. 1.9e-273;  
Matches 1251; Conservative 0; Mismatches 123; Indels 1; Gaps 1;  
QY 3 gtgatalcaaaagacgttgaagaatgaatttgaacttcaagtggtgaccactac 62  
|||||  
DB 122 GTTGATATCAAGAGAGTGAAGAAATGAAATTTGAAACTTCACGGGTGTCTACCCCTAC 181  
QY 63 agtactgccctgaacccttaacatccagcggttcgttagaaa-ccagctcaattctcttga 121  
|||||  
DB 182 ACTACTGCCCTGACCCCTTACATCCAGCGCTTATGAAACCCCACTCATTTCTCTCGTA 241  
QY 122 aagaatattatccagatcccatcgtcccaagagcaacaagaatattatccctcagtc 181  
|||||  
DB 242 AAGAAAGTTATTACCGGTGCGCATGTGCGACAGACCCGACAAAGTGTCTCTAGCC 301  
QY 182 cagaggtttccagacataltcttggaatttcttgaaacagcctatgttcaagtcacca 241  
|||||  
DB 302 CAGAGGTGTTCAGCATATCTGGATTTTCTGGAACAGCCTATGTCTGATACAGCCCA 361  
QY 242 ttgaacttgaacttgtagtgaacatcaagaatggtgtagcaaaacaagaattgagatta 301  
|||||  
DB 362 TCGACTTGAACTTTGTGGACGAGACATCAGAAATGTTGCAACAAACAGATTGAGATT 421  
QY 302 gtagtgaactgtatccgcatgagagctggagcttgaagtgaccctatgtgtagcagattga 361  
|||||  
DB 422 GCATGGATTGTATCCGATGACAGACTGACCTCATGATCCCATGTGGCCACAGTACA 481  
QY 362 cgaacctgggtctctctgaacaagcatgtgacagcaagattcaagaagctctctctgaccaca 421  
|||||  
DB 482 CCAACCTGGGGCTCTGGAAGGAGATGAGACACAGATTTCAGAAAGCGCTCTCATACCA 541  
QY 422 gtccctataacacagacacgcgcgaagaagtgtagcgcgccctcgccctagcagcgc 481  
|||||  
DB 542 GCCCTATTACACAGACCCATGCAAGAACAGGCTGACGCTCTGCTCTATGACACAC 601  
QY 482 cgaactcgaactctgtagtctctctctcaacacccgcatccctcccaacacagcattac 541  
|||||  
DB 602 CCAGCTCAACCTTCATGATGCCCTTTCTCCATCCCTCCCTGCTCCACACAGATTTAC 661  
QY 542 cagcgcgcagacagtttcgacgtgtcccttcacagcagtcgagcaacgcgcgaagtcgcacact 601  
|||||  
DB 662 CAGGCCACACAGACTTCGATGTGTCTCTCCACAGACGACACCGCAGTCAAGTCACT 721  
QY 602 gtagctatccatcgtgaagaactctactgccaattgcaagaagacatgcccattcc 661  
|||||  
DB 722 GGACGATTTCACCGCAACTGAAGAACTCTACTGCCAGATTGCCAAAGACCTCCCATCC 781  
QY 662 agatcaagtgtagtcccccaactcctcaagagagtgtagtcggcgccatgctgtctaca 721  
|||||  
DB 782 ACATCAAGGTGATGACCCACCCACACAGGGCGCGCTCATTTGTGCTAGTGCCTGTCTACA 841  
QY 722 aaaaagctgaagacgtlcaacgaggtgtgtgaagcgtgtgcccacaacatgaagtcgagcgtg 781  
|||||  
DB 842 AGAAAGCCAGCATGTGCACGAGGTTGTGAAGAGATGCTTAACACAGAGCTGAGGCGCG 901  
QY 782 aatcaagaaggaagacagattgcccctctcagtagcatattgtagttagaggggaacagcc 841  
|||||  
DB 902 ACTTCAATAGGAGACAGATTGGCCCTCCAGCATCTGATTTGAGTAGAAGGAACAGCC 961  
QY 842 atggccagatgtatagaagatcccatcaagaagaagaagagtgtagtgcgtgaccttaagac 901  
|||||  
DB 962 ATGCCAGTATGTAGAGATCTCTATACAGAGGAGGACAGAGCTGTGCTGTATGAGC 1021  
QY 902 caaccacagtttgacactgaattcaacagacagcttctgtacaatttcaatgtgtaacacagatt 961  
|||||  
DB 1022 CACACAGAGTTGGACATGATTCACAAACAGCTCTGTACAAATTTCAATGTCACAGACAGCT 1081  
QY 962 gtgttggaagatgaacgcggttccaatttataatcaatttactctggaaccacagagatg 1021  
|||||  
DB 1082 GTGTGAGAGATGAACCCGCTCCCAATTTTATATCTACTGTGGAACACAGAGATG 1141

QY	1022	ggaagctccctgggagcgagcgcgtctgtcttggaagcccgagctctgtcttgcccaagaagaagaa	1081
Db	1142	GGCAAGTCTCGGCGCGACGTTGCTTTCAGATCCCGGATCTCGCTTCCCAAGAAAGACCC	1201
OY	1082	ggaagcgagatgaagatagcatcagaagaagaaagtlctcgacaagtaacaagaacggtg	1141
Db	1202	GGAAGCGCGATGAAGACAGCATCAGAAAGACGCAAGATATCATGACACGCGCAAAAGAGCGCG	1261
OY	1142	atggtagaagaagcgccgcttctgtcagaacaacatggtatccagaatgaaatcattcatcaaga	1201
Db	1262	ATGTGACCAACAGCGCCCTTTCCTCGTCAAGATACCCACGGAAATCCAGATGACTTCATCAAGA	1321
OY	1202	aacgaagatcccccagatgatgaactgttataacttaccagaaggaagggcggtgaaactatg	1261
Db	1322	AACGGAGATCCCCAGATGATGATGACTGCTGTAACCTACCATGAGAGGCGCGAAGACTTATG	1381
OY	1262	aaatgctgttgaagatcaagaagatccctcgtgaacatccatgacgtactctcccaacacaa	1321
Db	1382	AAATCTCTCTCTCAAGATCAAGAGATCGCTCGAGCTCATGACATATCTCTCCACAGACAGA	1441
OY	1322	tgaagacgtacaggaacaacagcaacagcagcagcagcaactactactacaagaaca	1376
Db	1442	TGGAACGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACCAACTCTTCAGAAACA	1496
RESULT	12		
LOCUS	AF075435	1668 bp	mRNA
DEFINITION	Mus musculus TA*p63 beta mRNA, complete cds.		04-OCT-1998
ACCESSION	AF075435		
VERSION	AF075435.1	GI:3695091	
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Cranita; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 1668)		
AUTHORS	Yang, A., Kaphad, M., Wang, Y., Gillet, E., Fleming, M.D., Dotsch, V., Andrews, N.C., Caput, D. and McKeon, F.		
TITLE	p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities		
JOURNAL	Mol. Cell 2 (3), 305-316 (1996)		
MEDLINE	98448095		
AUTHORS	2 (bases 1 to 1668)		
TITLE	Yang, A., Kaphad, M., Caput, D. and McKeon, F.		
JOURNAL	Direct Submission		
FEATURES	Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240 Longwood Ave, Boston, MA 02115, USA		
source	Location/Qualifiers		
	1..1668		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
	/chromosome="16"		
	1..1668		
	/feature="transcription factor"		
	/note="second splice variant; related to p53 and p73"		
	/codon_start=1		
	/product="TA*p63 beta"		
	/protein_id="AAC62640.1"		
	/db_xref="GI:3695092"		
	/translation="MNFTSRCATLQCYCPDPIORLETPAFHSMKSEYRSMASOST		
	ONSRETPVPOHIDPLEPICSVPIELNEDVDESRGATNKEISMDEIRMQDDSD		
	LSPHMPQNTNIGLINSMDQIONGSSPSIPNDHANSYASAPSPSTSDALS		
	EPDITGRSGLVPEEPVQGETFTVLVNFKNSSCVGMMNRPLILVILETRDGOV		
	PPGCAVIRAMPYKKAHEVTVKAKPHNELSRRENEQIAPSHILIVERNIAOVV		
	PESAVISNTDIPROPHSEFVDSFOOSTASAMTWYETETKRTIXCOLAKCPLOIVMP		
	LGRCPEFARICAGPGRKRADEDSIRKQVDSANGDGTARKPEKRNHGILQMSIRK		
	TSQMSOSYGNSSPPLKNKSNMKLPSVQLINPOQRNALPTPTPEDEGMANIPMGV		
	HMMADNMGLNSTOALPPLPLSMPSRSHCTPPPTPPPTDCSIVRIWV"		
BASE COUNT	451 a 512 c 380 g 325 t		
ORIGIN			

Query Match	Local Similarity	Score	DB	Length
Best Local	91.4%	Pred. 2.9e-270		
Matches 123;	Conservative	0;	Mismatches 115;	Indels 1; Gaps 1
Qy	29	atgaattcttgaacttcacggtgtgtccaccctacagtactgccttgacccttacatccag	88	
Db	1	ATGAATTTTGAACCTTCACGGTGTGCCACCTTCACGATCTGCGCCGACCTTTCATATCCAG	60	
Oy	89	cglttctgtagaag-cccagctacttctcttcttgaaagaagtattatccgaatccacatg	147	
Db	61	CGTTTCATGAAACCCACAGCTCATTTCTCTGTGGAAAGAAAGTATTATACAGTCTGCCATG	120	
Oy	148	tcccaagacacacagacacaaatgaattctctcagttccaagagtttccagatattcggat	207	
Db	121	TCCGAGAGACACCCAGACACAGGATTCTCAGGCCAGAGGTCTTCCACCAATCTGGGAT	180	
Oy	208	ttctctgaaagcctatatgttcaagtcagccatgtactgtgaacttgtgttgaaacca	267	
Db	181	TTTTGGGAACGCTTATATGTCTAGTACAGCCCATGATGATCACTTGTGTGATGAACCT	240	
Oy	268	tcaagaagttgtgtgacaaaacaagattgagattagcatgtactgtatccgatccaagac	327	
Db	241	TCCGAAATATGTTGCAACAAACAAAGATTGAGATTAGCATGGATTGTATCCGATGCAAGAC	300	
Oy	328	tctgaacctgtgagtcgacccactgtgtgccaagttacagaaacctgtgtgtctcttgaaacagatg	387	
Db	301	TGAGACCTTCAGTGAACCCCATGTGGCCACAGTACAGCACTGGGGCTCTCTGAAACGATG	360	
Oy	388	gaaccaagcatctcgaagacgctctctgttccacagctccctataaacaagaacagcagac	447	
Db	361	GACCGACGATTTCGAAACAGGGCTCTCTCTCCACAGCCCTTACACACAGACACGACGACAG	420	
Oy	448	aacaagcgtcacagcgccccctcgcccctacagcaagccaagctcaactctogaagctctctc	507	
Db	421	AATFACGTGAGAGGGCCCCCTCGCCTTAGTGCACAGCCAGCTCCACTTTGATGCTCCCTCT	480	
Oy	508	ccataaccgcacatccctctccaacaccgactaacccagggccccaagattctgaagtgtcc	567	
Db	481	CCATCCCCCTGCATTCCTCTCCACACAGATTACCCGGGCCACACAGCTTCCATTGTGTCC	540	
Oy	568	ttccagacagtcgagcaccgcgaagtctggaccaactctgagcgtatctcaactgaaatgaana	627	
Db	541	TTTCCAGCATCAAGACACGTCCCAAGTCAAGCCACTGTGACCTGATTCACCCAGTGAAGAG	600	
Oy	628	ctctactgcnaaatttgaagaagatctgcccactccaagtccaagttgattgagcccaactct	687	
Db	601	CTTACTGTCCCAATTGTGCAGACATGTGCCCTTCACAGTACAGGTGATGACCCACCCCCA	660	
Oy	688	caagagagcgttatctacgcgcacatgtctcttacaanaaaagtctagacagtlcaacgagtg	747	
Db	661	CAGGGGCTGTATTATCCGTGCCATGCTGTCTTACAAAGAAAGCTGAGATGACCGAGGTT	720	
Oy	748	gtgaagcgggtgcccacaacatlgagctgagccgtgaattcaacgaaggagacagattgtccct	807	
Db	721	GTAAGAACGATGCCCTAACCATGAGCTGAGCCGTGATGATTCATGTAGGAGACAGATTGGCCCT	780	
Oy	808	cctaagcatattgattctggatgaagggagaaagccatccccaatgtfagaagaatccacatc	867	
Db	781	CCAGATCATCTGATTGAGATTGAAGAGAAACGCCATGCCATGATGTGAGAAATCTCTATC	840	
Oy	868	acaggaagacagagtgctgtgttacctatctatgacccaccccaagtttgcaactgaaatccag	927	
Db	841	ACGGGAAGGACAGCGCTGTGCTTCCCTTATGAGCCACACAGTGTGGCACTGTAATTCACA	900	
Oy	928	acagctctgtacaaattcattgtgtacagcagttgtgtgtgaaggtatgaaacgcgcgtcca	987	
Db	901	ACAAGTCTCTATCAATTTTCATGTGTAAACACACACTCTCGTGAAGGAATGAACAGACGTCCA	960	
Oy	988	atttatactgttactcttggaacccaagatgagcagaatccctgggacgcagcgtgtctt	1047	
Db	961	ATTTTATCATCTGTACTCTGGAACACAGATGTGGGCAAGTCTGTGGGCCGACGCTGCTTT	1020	

Oy 1048 gagcccgatctgctctcccaagaagacaggaagcgatgatacatcaga 1107  
|||||  
Db 1021 GAGGCCCGGATCTGCTTCCGCCAAGAGAGCGGAGGCGATGAGACGATCAGA 1080  
Oy 1108 aagagcaagttcgagacagcaagaacggtgtagtaagcgccgcttgcag 1167  
|||||  
Db 1081 AAGCAGCAAGTATCGACAGCGCAAGAACGCGATGTACGAACGCCCTTCCGTCAG 1140  
Oy 1168 aacacacgtatccatgatactgacacaaagaagaagctcccgatgatactc 1227  
|||||  
Db 1141 AATACACACGGAAATCCATATGATCTTCATCAAGAAACGAGATCCCGATGATAGATCG 1200  
Oy 1228 ttatactacagtgagggccgtgagacttaagaatgctgtgaagatacaagatcc 1287  
|||||  
Db 1201 CTGTAACCTACAGTACAGAGGTGTGAGACGTACGATGCTTCTGAAGATCAAAAGTCA 1260  
Oy 1288 ctggaactcatgtagtacctctcagacacaaatgaaagctagaggaacagcaacag 1347  
|||||  
Db 1261 CTGAGCTCATGTCACTACTCCCTCAGACACAGATCGAAACGTACAGGACGACGACGAG 1320  
Oy 1348 cagcagcagcagcacttacttcaagaaca 1376  
|||||  
Db 1321 CAGCAGCACGACCTACTTCAAGAACCA 1349

RESULT 13  
AF075436  
LOCUS AF075436 2043 bp mRNA  
DEFINITION Mus musculus TA-p63 alpha mRNA, complete cds.  
ACCESSION AF075436  
KEYWORDS GI:3695093  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 2043)  
AUTHORS Yang, A., Kaghad, M., Wang, Y., Gillett, E., Fleming, M.D., Dotsch, V.,  
Andrews, N.C., Caput, D. and McKee, F.  
p63, a p53 homolog at 3q27-29, encodes multiple products with  
transactivating, death-inducing, and dominant-negative activities  
Mol. Cell 2 (3), 305-316 (1998)  
98448095

TITLE  
JOURNAL  
MEDLINE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
SOURCE  
1. 2043  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/chromosome="16"  
1. 2043  
/function="transcription factor"  
/note="third splice variant; related to p53 and p73"  
/codon\_start=1  
/product="TA-p63 alpha"  
/protein\_id="AAC6264.1"  
/db\_xref="GI:3695094"  
/translation="MNETSRCATLQYCPDPYIORFIETPAHFSWRESYRSASOST  
OTSELEPVEFOHIMDFLEOPICISYVPELNPBPSPSNGANPKIETIMDCIRMODSD  
LSDPMPOYTLGILSMDOIONSSSTSYNDHONSTANPEYKPOPSSTDALS  
PSPAIPSTNIDPGHSEFVSFOOSTAKSATWYSTEKLKLYCOIAKCPJOIKVMP  
PPGAVIKAMPVYKAEHTEVYKCPNHELISRENEQIAPPSHLIIVENSHAOY  
EDPTGROSVLYPEPPQVTEFTVLNFCNSCYGAMRRPILITVLETBGOY  
LGRCEFIACAGDRKADEDSIRKQVSDSAKNGDGRKPRONTHGIOMTSIK  
RRSDDELLYLVGRETVELIKIKESLEIMQYLPHTITRYROOOOHOHLIOK  
TSMOSOSYGNSSPKMNSMKNLPSQILNQORALPTTTPBEMGANIPMGT  
HPMAGDMNGSLPTOALPPPLSMPSICTPPPTDCTSVSLARLSCSDLYFT  
TGGLTYYQIEHYSMDLALSLKIPQFNHAIWKGLDRLQHLSSPHLLRTPGAS  
TVSVSSSTRBERYDAVRFRLRQTIISPPDEWDFNFDMDSRANKOORKEGE"

CDS  
BASE COUNT 536 a 622 c 471 g 414 t

ORIGIN

Query Match 40.9%; Score 1153; DB 94; Length 2043;  
Best Local Similarity 91.4%; Pred. No. 3e-270;  
Matches 1233; Conservative 0; Mismatches 115; Indels 1; Gaps 1;

Oy 29 atgaatttgaacttaacaggtgtgtccaccataagtaactgtcccttacatccag 88  
|||||  
Db 1 ATGAATTTTGAACCTTACAGGTGTGCTCCACCTTACAGTACTGCGCCGACCTTACATCCAG 60  
Oy 89 cgttcgttagaaa-ccagatcattctctcttggaaaagaagtlatlacgataccacatg 147  
|||||  
Db 61 CGTTTCATAGAAACCCCGAGCTCATTTCTGTGGAAGAAGATATTACAGATCTGCATG 120  
Oy 148 tcccaagagcaacagacaatgaattctcagtcagagaggtttccagatatactggat 207  
|||||  
Db 121 TCGCAGAGCACCACAGACAAAGCGATTCTTCACCGCAGAGGTCTTCACCATATCTGGGAT 180  
Oy 208 ttcttggaacagcctatatgttcagttcagagccatctgacttgacttgacttgatgatacca 267  
|||||  
Db 181 TTTCTGGAACACCTTATATGCTCACTACAGCCCATCGAATTAACTTGTGATGATACCT 240  
Oy 268 tcagaagatggtgcgacaacaagaatgagatlaagcatgtagctgataccgcatgaggagc 327  
|||||  
Db 241 TCCGAATAATGTCGCAACAACAAGATTGAGATTAGCATGATGATTCGCGATGCAAGAC 300  
Oy 328 tcggaactgagatgagcccatgtgtgccaagatgacagaactggtggctcctgaacagatg 387  
|||||  
Db 301 TCAGACCTCAGTGAACCCCATGTGGCCACAGTACAGAACCTTGGGCTCTCTGAACAGCATG 360  
Oy 388 gaccagcagatccagaagcgctcctcgtccacagctccctataacaagaacacagcag 447  
|||||  
Db 361 GACCGACAGATTTCAGACAGCGCTCTCTGTCACAGCCCTTAAACACAGACACGACAG 420  
Oy 448 aacagcgtlcaagcgccctcgcctcagcagacagccagctccactcgtatctctct 507  
|||||  
Db 421 AATAGCGTGAAGCGCGCGCTCGGCTATGACAGCCAGCTCCACCTTGATGATGCGCTCT 480  
Oy 508 ccatacccgcatccctcccaacacagactacccaagccagccagcagatgtcgatgtcc 567  
|||||  
Db 481 CCATGCCCTGCTATCCCTCCCAACACAGATACCGGGGCCACACAGCTTCATGTCCTCC 540  
Oy 568 ttccagcagtgagagcagcagcagctcgccacttgagctatccacttgaaactgaaaga 627  
|||||  
Db 541 TTCCAGCACTCAAGCACTGCCAAGTCAAGCTACCTGAGCTATTCACGCACTGAAGAAG 600  
Oy 628 cctactgcaaatctgcaagacatgccccatccagatcaagtgatgacccacctct 687  
|||||  
Db 601 CTGTACTGCCAATTTGCGAAGACATGCCCATCCAGATCAAGTGATGACCCACCCCA 660  
Oy 688 caggagagctgtatccgcgcacatgacctgtctacaaaaaagctgagcaactgagagtg 747  
|||||  
Db 661 CAGGCGGCTGTTATCCGTCCTGCTGCTTCAAGAAAGCTGACATGTCACCGAGTT 720  
Oy 748 gtgaagcgtgtgcccacatgagctgagcgttgatgaagaaggaagaattgacct 807  
|||||  
Db 721 GTGAACGATGCTTACCATGAGCTGAGCGCTGAGTTAAAGAGGAGAGATGCGCT 780  
Oy 808 cctagtcatttgatcagatgaagggaacacagccatgcccaglatgtagaagaatccatc 867  
|||||  
Db 781 CCAGCATCTGATTCGATGATGAAGGAACACGCAATGCCCAATATGTAGAATCTTATC 840  
Oy 868 acaggaagacagatgctgtgctgtaacctatgagcaacccaggttggcaactgaatcag 927  
|||||  
Db 841 ACGGGAAGCAAGAGGTGCTGCTCTTATGAGCAACACAGAGTTGGCTCAATTCACA 900  
Oy 928 acagctgttaaatcttaacatggtgaagcagctgtgtgtggaggaataaaccgctgca 987  
|||||  
Db 901 ACAGTCTCTTACAAATTTCTATGTGTAACACACACTGCGTGAGGAGATGACAGAGCTCA 960  
Oy 988 atttaatatgttactcttgaaaccagaagatggcgcaagctcctggcgaagcgtctt 1047  
|||||









GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2001, 22:04:29 ; Search time 221.11 Seconds  
(without alignments)  
7996.793 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816  
Sequence: 1 tgcgtatatacaagaacagt.....gcattctgtttaagaaga 2816

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq\_0601.\*

```
1: /cgnl_9/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /cgnl_9/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /cgnl_9/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /cgnl_9/gcgdata/geneseq/geneseqn/NA1983.DAT.*
5: /cgnl_9/gcgdata/geneseq/geneseqn/NA1984.DAT.*
6: /cgnl_9/gcgdata/geneseq/geneseqn/NA1985.DAT.*
7: /cgnl_9/gcgdata/geneseq/geneseqn/NA1986.DAT.*
8: /cgnl_9/gcgdata/geneseq/geneseqn/NA1987.DAT.*
9: /cgnl_9/gcgdata/geneseq/geneseqn/NA1988.DAT.*
10: /cgnl_9/gcgdata/geneseq/geneseqn/NA1989.DAT.*
11: /cgnl_9/gcgdata/geneseq/geneseqn/NA1990.DAT.*
12: /cgnl_9/gcgdata/geneseq/geneseqn/NA1991.DAT.*
13: /cgnl_9/gcgdata/geneseq/geneseqn/NA1992.DAT.*
14: /cgnl_9/gcgdata/geneseq/geneseqn/NA1993.DAT.*
15: /cgnl_9/gcgdata/geneseq/geneseqn/NA1994.DAT.*
16: /cgnl_9/gcgdata/geneseq/geneseqn/NA1995.DAT.*
17: /cgnl_9/gcgdata/geneseq/geneseqn/NA1996.DAT.*
18: /cgnl_9/gcgdata/geneseq/geneseqn/NA1997.DAT.*
19: /cgnl_9/gcgdata/geneseq/geneseqn/NA1998.DAT.*
20: /cgnl_9/gcgdata/geneseq/geneseqn/NA1999.DAT.*
21: /cgnl_9/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /cgnl_9/gcgdata/geneseq/geneseqn/NA2001.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2816	100.0	2816	20 AA257770	Human p51 encoding
2	2816	100.0	2816	21 AAC66029	Human lung cancer
3	1376	48.9	2270	20 AAC25771	Human p51 encoding
4	1376	48.9	2270	21 AAC66028	Human lung cancer
5	1364	48.4	4846	21 AA243913	Human KET CDNA. H
6	1364	48.4	4849	21 AAC66031	Human lung cancer
7	1346	47.8	1347	20 AAX58574	Human cell regulat
8	1232	43.8	1551	20 AAX58573	Human cell regulat
9	1232	43.8	1551	21 AAC66033	Human lung cancer
10	1232	43.8	1926	20 AAX58572	Human cell regulat
11	1218.2	43.3	1452	20 AAX58580	Mouse cell regulat

12	1154.6	41.0	2043	20	AAX58577	Human cell regulat
13	1143.6	40.6	1182	20	AAX58576	Human cell regulat
14	1031.2	36.6	2082	20	AA227674	Human p40 coding s
15	1031.2	36.6	2082	21	AAC66030	Human lung cancer-
16	1031.2	36.6	4708	21	AA243912	Rat KET cDNA. Rat
17	1028.6	36.5	1386	21	AAC66032	Human lung cancer-
18	1028.6	36.5	1761	21	AAC65875	Human cell regulat
19	1027.6	36.5	4655	21	AAC65887	Human lung cancer-
20	1026.4	36.4	2820	21	AAC66027	Human lung cancer-
21	951.2	33.8	1170	20	AAX58583	Mouse cell regulat
22	922.8	32.8	4643	20	AA224648	Human lung tumor a
23	884.6	31.4	1386	20	AAX58582	Mouse cell regulat
24	884.6	31.4	1761	20	AAX58581	Mouse cell regulat
25	466.8	16.6	1594	21	AA249690	Human p73 protein
26	466.8	16.6	1817	18	AAV01505	Human p53 tumour s
27	466.8	16.6	1870	18	AAV01504	Human p53 tumour s
28	466.8	16.6	2156	18	AAV01498	Human p53 tumour s
29	466.4	16.6	1521	18	AAV01503	Human p53 tumour s
30	466.4	16.6	1764	18	AAV01502	Human p53 tumour s
31	463.8	16.5	2034	18	AAV01497	Monkey p53 tumour
32	463.8	16.5	2874	18	AAV01496	Monkey p53 tumour
33	458.6	16.3	2040	18	AAV01499	Mouse p53 tumour s
34	308	10.9	308	22	AAF25912	Human tumor suppre
35	244.2	8.7	1215	17	AAT32836	Human p53 ECOR1-Sa
36	242.6	8.6	1181	16	AAO97854	Human p53 CDNA. H
37	242.6	8.6	1181	20	AA227570	Human p53 coding s
38	242.6	8.6	1181	21	AA61625	CDNA encoding huma
39	242.6	8.6	1181	21	AAA29399	DNA disclosed in p
40	242.6	8.6	1182	15	AAO67884	Human p53 DNA. 5Y
41	242.6	8.6	1182	17	AAT29719	Wild type p53 gene
42	242.6	8.6	1182	20	AA208529	Human p53 gene. H
43	242.6	8.6	1185	17	AAT27665	Human p53 gene seq
44	242.6	8.6	1203	17	AAT27663	Human p53 gene seq
45	242.6	8.6	1209	18	AAT86219	Human p53 protein

## ALIGNMENTS

RESULT 1	
AA257770	
ID	AA257770 standard; CDNA: 2816 BP.
AC	AA257770;
XX	
DT	07-JAN-2000 (first entry)
XX	
DE	Human p51 encoding CDNA A.
XX	
KW	Human; p51; p53 related gene; cell proliferation; regulation; cancer;
KW	tumour suppression; diagnosis; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	polyA_signal
FT	Location/Qualifiers
FT	/*tag=a
FT	2786..2791
FT	/*tag=b
PN	
XX	
PD	W09950412-A1.
XX	
PD	07-OCT-1999.
XX	
PF	24-MAR-1999; 99WO-JP01512.
XX	
PR	27-MAR-1998; 98JP-0100467.
XX	
PA	(SAKA) OTSUKA PHARM CO LTD.
PA	(IKAWA) IKAWA Y.
XX	
PI	Ikawa Y, Ikawa S, Obinata M;
XX	

DR WPI: 1999-591318/50.  
 DR P-PSDB: AAY45246.  
 XX  
 PT New p53 related human gene p51, useful for diagnosis, investigation and  
 PT treatment of cancers and screening for potential cell proliferation  
 PT agents -  
 XX  
 PS Claim 3: Page 148-151: 163pp; Japanese.  
 XX  
 CC The present sequence represents a human p51 gene, which is related to  
 CC p53 and has cell proliferation regulation and tumour suppression  
 CC activity. The p51 gene can be used in the investigation, diagnosis and  
 CC treatment of diseases such as cancer, with which the p53 family cell  
 CC proliferation regulation is associated. The p51 protein may be used for  
 CC screening potential agonists and antagonists of its regulatory function,  
 CC for use as drugs,  
 CC  
 XX  
 XX  
 SQ Sequence 2816 BP; 781 A; 658 C; 619 G; 758 T; 0 other;

Query Match 100.0%; Score 2816; DB 20; Length 2816;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcgttgatatacaagaagctgaagaaatgaattgaacttcacggtgtgccacct 60  
 DB 1 tcgttgatatacaagaagctgaagaaatgaattgaacttcacggtgtgccacct 60  
 QY 61 aacgctcctcctgacaccttacatccagcttcctgagaacaccccgcttctcttg 120  
 DB 61 aacgctcctcctgacaccttacatccagcttcctgagaacaccccgcttctcttg 120  
 QY 121 aagaagaatattacacgataccatcctatgctccagagcacacaatgaattctcagt 180  
 DB 121 aagaagaatattacacgataccatcctatgctccagagcacacaatgaattctcagt 180  
 QY 181 ccaagaggtttccagagatctcggagattctcggaaacgctatatgtcagttcaagcc 240  
 DB 181 ccaagaggtttccagagatctcggagattctcggaaacgctatatgtcagttcaagcc 240  
 QY 241 attgacttgaaacttggtgatgaacacatcagaagatgtgagcacaacaagaattagatt 300  
 DB 241 attgacttgaaacttggtgatgaacacatcagaagatgtgagcacaacaagaattagatt 300  
 QY 301 agcatgagactgtatccgcgacatgcagactgcgacccatgagcccatggtgcacagatc 360  
 DB 301 agcatgagactgtatccgcgacatgcgacccatgagcccatggtgcacagatc 360  
 QY 361 acgaacactgggctcctcgaacagcaltgacccagcagattcagaagcgtctcctgcacac 420  
 DB 361 acgaacactgggctcctcgaacagcaltgacccagcagattcagaagcgtctcctgcacac 420  
 QY 421 agtccctataacacagacacgcgcagaaacagtcacagcgccctcgcctacgcacag 480  
 DB 421 agtccctataacacagacacgcgcagaaacagtcacagcgccctcgcctacgcacag 480  
 QY 481 cccagctcaaccttgatgctctctcctcaatcaccgcgcacatccctcacaacacgactac 540  
 DB 481 cccagctcaaccttgatgctctctcctcaatcaccgcgcacatccctcacaacacgactac 540  
 QY 541 ccaagcccgacagatttgagcgtctcctcgaacagtcagagacgcgcaagtgcgacac 600  
 DB 541 ccaagcccgacagatttgagcgtctcctcgaacagtcagagacgcgcaagtgcgacac 600  
 QY 601 tggagatattccactgaaactgaagaactctactcgaatgtcaagaacagatgcccactc 660  
 DB 601 tggagatattccactgaaactgaagaactctactcgaatgtcaagaacagatgcccactc 660  
 QY 661 cagatcaagtgatgacccacacccctcctcaaggagagctgtatccgcgcagctgtctac 720  
 DB 661 cagatcaagtgatgacccacacccctcctcaaggagagctgtatccgcgcagctgtctac 720  
 QY 721 aaaaagctgagcagcgtacagcaggttggtgaagcgtgcacccaacatgagactgacgct 780

DB 721 aaaaagctgagcagcgtacagcaggttggtgaagcgtgcacccaacatgagactgacgct 780  
 QY 781 gaattcaagaagagacagatgcccctcctcctagctatgattcgatgagaggaacagc 840  
 DB 781 gaattcaagaagagacagatgcccctcctcctagctatgattcgatgagaggaacagc 840  
 QY 841 catgcccagatgatagaatcccatcacaaggaagacagatgctgtgacttaag 900  
 DB 841 catgcccagatgatagaatcccatcacaaggaagacagatgctgtgacttaag 900  
 QY 901 ccacccaggttgagcactgaattcacaagacagctgtgataatltcaatgltgaacagcagt 960  
 DB 901 ccacccaggttgagcactgaattcacaagacagctgtgataatltcaatgltgaacagcagt 960  
 QY 961 tgtgttgagaggaatgaacgcgcgtccaatlttaacatgttactctggaacacagagat 1020  
 DB 961 tgtgttgagaggaatgaacgcgcgtccaatlttaacatgttactctggaacacagagat 1020  
 QY 1021 gggcaagctcctgagcgcgcgtctgttgaagcccgatctgtctgcccaggaagagac 1080  
 DB 1021 gggcaagctcctgagcgcgcgtctgttgaagcccgatctgtctgcccaggaagagac 1080  
 QY 1081 aggaagcgcgatagaagatagcatcagaagaagcagcagtttcgagacagtacaagaagcgt 1140  
 DB 1081 aggaagcgcgatagaagatagcatcagaagaagcagcagtttcgagacagtacaagaagcgt 1140  
 QY 1141 gatgttaagaagcgcgcgtcttcgtcagaacacacatggtatccagatgaatccatcaag 1200  
 DB 1141 gatgttaagaagcgcgcgtcttcgtcagaacacacatggtatccagatgaatccatcaag 1200  
 QY 1201 aacgcaagatcccccagatgatactgtatcactacagagagagcggtgagacttat 1260  
 DB 1201 aacgcaagatcccccagatgatactgtatcactacagagagagcggtgagacttat 1260  
 QY 1261 gaaatgctgttgaagaatcaagaagctcccttggaactcaltgcagatcctcctcacaacaca 1320  
 DB 1261 gaaatgctgttgaagaatcaagaagctcccttggaactcaltgcagatcctcctcacaacaca 1320  
 QY 1321 attgaaagcttcaagcacaacacagacagacagacacacacacacacacacacacac 1380  
 DB 1321 attgaaagcttcaagcacaacacagacagacagacacacacacacacacacacacac 1380  
 QY 1381 ctttaagcctgtccttaagaagaatgagctgtgagcccggaagaagaatcccaaaacatct 1440  
 DB 1381 ctttaagcctgtccttaagaagaatgagctgtgagcccggaagaagaatcccaaaacatct 1440  
 QY 1441 gaagctctcctttagacatcccaagcccccaaacagatagtgtaaccatlagagccctatc 1500  
 DB 1441 gaagctctcctttagacatcccaagcccccaaacagatagtgtaaccatlagagccctatc 1500  
 QY 1501 tctaatattgaagtggtgtgtgttattccatgtgtatgatagtgagtggtgtgtgta 1560  
 DB 1501 tctaatattgaagtggtgtgtgttattccatgtgtatgatagtgagtggtgtgtgta 1560  
 QY 1561 tgtgtgtgctgtgtatcattcagccctcaataaacagagacttgaagaacacttgcgcacaga 1620  
 DB 1561 tgtgtgtgctgtgtatcattcagccctcaataaacagagacttgaagaacacttgcgcacaga 1620  
 QY 1621 cccaactgctcaaaagcacaagcccaactagtgagagaatcctttgaagggaactcaaacct 1680  
 DB 1621 cccaactgctcaaaagcacaagcccaactagtgagagaatcctttgaagggaactcaaacct 1680  
 QY 1681 ttacaagaagaagatgtttctgcagagatttgatccttaagacgcgcagctgtgtgtgag 1740  
 DB 1681 ttacaagaagaagatgtttctgcagagatttgatccttaagacgcgcagctgtgtgtgag 1740  
 QY 1741 gaacacactgtgtgtcctgtgagacttctgttctcctggaagagaggttcaggtgagg 1800  
 DB 1741 gaacacactgtgtgtcctgtgagacttctgttctcctggaagagaggttcaggtgagg 1800  
 QY 1801 gaaagggcatlaagaatgttattatggaaccccttctgctctctctgtgttttcttaa 1860



Qy	301	agcatctgactgtatctccgcatctgacagagatctcgagactgtagttgaaaccccatgvtgcccacagttac	360
Db	301	agcatctgactgtatctccgcatctgacagagatctcgagactgtagttgaaaccccatgvtgcccacagttac	360
Qy	361	acgaacactggagctctcttgaaacagcatctgaaacagagattctgaacacgctctctgtccacc	420
Db	361	acgaacactggagctctcttgaaacagcatctgaaacagagattctgaacacgctctctgtccacc	420
Qy	421	agttccataaacaagacaagacgcgcgaagaacagcgtacacgctgcgccttcacgcagacag	480
Db	421	agttccataaacaagacaagacgcgcgaagaacagcgtacacgctgcgccttcacgcagacag	480
Qy	481	cccaagctcccaactcttgatgtctctctccatccatcccgccatccctcccaacacgcagttac	540
Db	481	cccaagctcccaactcttgatgtctctctccatccatcccgccatccctcccaacacgcagttac	540
Qy	541	ccaaagcccgacacagttcttcgacgtgtctcttcacagacttgaaagacacgcgcgaagtcgcacc	600
Db	541	ccaaagcccgacacagttcttcgacgtgtctcttcacagacttgaaagacacgcgcgaagtcgcacc	600
Qy	601	tgagcgtattccactctgaactctgaaagaactctatctccaaatttgaaagaacatgcccacatc	660
Db	601	tgagcgtattccactctgaactctgaaagaactctatctccaaatttgaaagaacatgcccacatc	660
Qy	661	cagaatcaaggtgactgaccccaactcctctcagggagctgtttatccgcgcgcacatgacctgtctac	720
Db	661	cagaatcaaggtgactgaccccaactcctctcagggagctgtttatccgcgcgcacatgacctgtctac	720
Qy	721	aaaaaagctgaagcactgacgtacacgcgcgcgtgtgtgaaagcgtgcccccaacatgagctgagcgcgt	780
Db	721	aaaaaagctgaagcactgacgtacacgcgcgcgtgtgtgaaagcgtgcccccaacatgagctgagcgcgt	780
Qy	781	gaattcaacaagagagacagatctgccccctccatgactttgatctgaagtgaaggggaaacagc	840
Db	781	gaattcaacaagagagacagatctgccccctccatgactttgatctgaagtgaaggggaaacagc	840
Qy	841	caatgccagttactgtagaagaatcccatcacagaagaacagagtgvtgctgtactcttatgag	900
Db	841	caatgccagttactgtagaagaatcccatcacagaagaacagagtgvtgctgtactcttatgag	900
Qy	901	ccaccccaaggtctgacatctgattcatcagacagctgtgtcaaatctatctgtgaacagagcgt	960
Db	901	ccaccccaaggtctgacatctgattcatcagacagctgtgtcaaatctatctgtgaacagagcgt	960
Qy	961	tgctgtgagagagatgaaacgcgcgtcccaatttaactatgttactcttgaaaccaagagat	1020
Db	961	tgctgtgagagagatgaaacgcgcgtcccaatttaactatgttactcttgaaaccaagagat	1020
Qy	1021	gggcagaagctcccgagcgcgcgcgtcttgagagcccgagatctgagcttgcccgaggaagagac	1080
Db	1021	gggcagaagctcccgagcgcgcgcgtcttgagagcccgagatctgagcttgcccgaggaagagac	1080
Qy	1081	aggaagcgcggaatgaaagatagcatacagaagaacagttctcgagacgtacaaagaacgcgt	1140
Db	1081	aggaagcgcggaatgaaagatagcatacagaagaacagttctcgagacgtacaaagaacgcgt	1140
Qy	1141	gattggttaagaaagcgcgcgcgttctgttcgaagaacacatgattcccaatgaaatgaaatccatgaag	1200
Db	1141	gattggttaagaaagcgcgcgcgttctgttcgaagaacacatgattcccaatgaaatgaaatccatgaag	1200
Qy	1201	aaacgaagaatccccaagatagtatgacttacttaaccagtgaggggcgtgagagattat	1260
Db	1201	aaacgaagaatccccaagatagtatgacttacttaaccagtgaggggcgtgagagattat	1260
Qy	1261	gaaatgctgtgtgaaagatcaaaagagctccctvgaaactatgvcagttacctctccagcaaca	1320
Db	1261	gaaatgctgtgtgaaagatcaaaagagctccctvgaaactatgvcagttacctctccagcaaca	1320
Qy	1321	attggaagctaacagagcaacagcaacagcaacagcaacagcaacattctccagaaaaacatctc	1380
Db	1321	attggaagctaacagagcaacagcaacagcaacagcaacagcaacattctccagaaaaacatctc	1380
Qy	1381	ctttcaagcctcttcacagatgaaattgtgtgtgaaagcccccggagagaactcccaaaaacatct	1440

D	b	1381	ctttagcctgctttaggaagagagcttctgttgagcccgagagaaactccaaaacatct	1440
Q	y	1441	gacgcttcctttagaacattccaagcccccacacgatcagtgtaaccaatagagccatac	1500
D	b	1441	gacgcttcctttagaacattccaagcccccacacgatcagtgtaaccaatagagccatac	1500
Q	y	1501	tctataattttaagtggtgtgtgttgaatttcgatgtgatagtatgtatgtgtgtgtgtat	1560
D	b	1501	tctataattttaagtggtgtgtgttgaatttcgatgtgatagtatgtatgtgtgtgtat	1560
Q	y	1561	tgtgtgtcgtgtgtatcatccctccataaaacagagacttgaagacacttggctcaga	1620
D	b	1561	tgtgtgtcgtgtgtatcatccctccataaaacagagacttgaagacacttggctcaga	1620
Q	y	1621	cccactgtctaaagacacaaagccacatagtagaggaattcttttgaagagactcaaacct	1680
D	b	1621	cccactgtctaaagacacaaagccacatagtagaggaattcttttgaagagactcaaacct	1680
Q	y	1681	ttcaagaagaagatcttctctgacaactctgtatcccttagaccggccattgtgtgtgtag	1740
D	b	1681	ttcaagaagaagatcttctctgacaactctgtatcccttagaccggccattgtgtgtgtag	1740
Q	y	1741	gaaccaactgtgttctgtctgttgagccttctgttctgttccctgtggaggggtccagtgtag	1800
D	b	1741	gaaccaactgtgttctgtctgttgagccttctgttctgttccctgtggaggggtccagtgtag	1800
Q	y	1801	gaagaaggagcatcaaatgttctatctgaaaccccttctctcctctctctgttcttctctaa	1860
D	b	1801	gaagaaggagcatcaaatgttctatctgaaaccccttctctcctctctctgttcttctctaa	1860
Q	y	1861	aattccagggagagccttttgagcaggtctcaaatcaaatgaatgtccttttaagaaaggag	1920
D	b	1861	aattccagggagagccttttgagcaggtctcaaatcaaatgaatgtccttttaagaaaggag	1920
Q	y	1921	aaaaaagttgttatgtctgtctgcatcaagaatgttgaatgacatgaagagactcaatcaga	1980
D	b	1921	aaaaaagttgttatgtctgtctgcatcaagaatgttgaatgacatgaagagactcaatcaga	1980
Q	y	1981	ccctttaaagtctgtgtcatalgtataataatctgcaagtagtaagaaacgaaaggtgtcaagt	2040
D	b	1981	ccctttaaagtctgtgtcatalgtataataatctgcaagtagtaagaaacgaaaggtgtcaagt	2040
Q	y	2041	tactgtctggcagcgagagatcatctaccacaaagaatcaactctgtgtgtgtgtgtgtgtc	2100
D	b	2041	tactgtctggcagcgagagatcatctaccacaaagaatcaactctgtgtgtgtgtgtgtgtc	2100
Q	y	2101	ttctgttagagactgtcatatttgtgtgtcctccctccatgtgtatgtagaacaattctaat	2160
D	b	2101	ttctgttagagactgtcatatttgtgtgtcctccctccatgtgtatgtagaacaattctaat	2160
Q	y	2161	gctgtgtactgctctctgcacatgtatgtgtgacatctgtatgtgtgtgtgtgtgtgtt	2220
D	b	2161	gctgtgtactgctctctgcacatgtatgtgtgacatctgtatgtgtgtgtgtgtgtgtt	2220
Q	y	2221	catgaaacccctgtgaagacctactatacaaaaaactgttgttggccccaatgacagtga	2280
D	b	2221	catgaaacccctgtgaagacctactatacaaaaaactgttgttggccccaatgacagtga	2280
Q	y	2281	ctcaatttgtgtctttaatagaagaagcaaatccaccccgtaatatgtgcccctaagtgt	2340
D	b	2281	ctcaatttgtgtctttaatagaagaagcaaatccaccccgtaatatgtgcccctaagtgt	2340
Q	y	2341	tgtttaccatattcaaaactcaaaatagaatattgtagagccctcccaaaaactgtgtat	2400
D	b	2341	tgtttaccatattcaaaactcaaaatagaatattgtagagccctcccaaaaactgtgtat	2400
Q	y	2401	aatttgttaataatagagctctatccctcaagctactacataaaacagacatata	2460
D	b	2401	aatttgttaataatagagctctatccctcaagctactacataaaacagacatata	2460
Q	y	2461	ctgataactgttcaagtgtcatatttagccagggacttaagttttagtaagtgaaatccaagc	2520
D	b	2461	ctgataactgttcaagtgtcatatttagccagggacttaagttttagtaagtgaaatccaagc	2520

Db 2461 ctgatactgttcagtgacatttagccagagacttactgttttgagtaagtgagatccaagc 2520  
Oy 2521 agacgtgtaaaatcacgacctccctgactgtgaaattaaagattgaaggtgtagactact 2580  
|||||  
Db 2521 agacgtgtaaaatcacgacctccctgactgtgaaattaaagattgaaggtgtagactact 2580  
Oy 2581 tctcttttttactcaaaagtttagagaatcctgtttcttccattttaaaaaatatt 2640  
|||||  
Db 2581 tctcttttttactcaaaagtttagagaatcctgtttcttccattttaaaaaatatt 2640  
Oy 2641 ttaagataatgacataaagactttaaaatgtctccctccatcttccacaccagc 2700  
|||||  
Db 2641 ttaagataatgacataaagactttaaaatgtctccctccatcttccacaccagc 2700  
Oy 2701 caccgacctatcttctgtacacaagaatgtattctgttttagagctgtgtc 2760  
|||||  
Db 2701 caccgacctatcttctgtacacaagaatgtattctgttttagagctgtgtc 2760  
Oy 2761 ttgttgatgtgtgatttcaatttcaataaactttgcatctgtgtttaaaagaa 2816  
|||||  
Db 2761 ttgttgatgtgtgatttcaatttcaataaactttgcatctgtgtttaaaagaa 2816

RESULT 3

AA25771  
ID AA25771 standard; CDNA: 2270 BP.

XX AC AA25771:

DT 07-JAN-2000 (first entry)

DE Human p51 encoding cDNA B.

XX Human p51: p53 related gene; cell proliferation; regulation; cancer;

KH tumour suppression; diagnosis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 145..2070

FT /\*tag= a

XX MO9950412-A1.

XX PD 07-OCT-1999.

XX PF 24-MAR-1999; 99WO-JP01512.

XX PR 27-MAR-1998; 98JP-0100467.

XX PA (SAKA ) OTSUKA PHARM CO LTD.

PA (IKAWA/) IKAWA Y.

PI Ikawa Y, Ikawa S, Obinata M;

XX DR WPI: 1999-591318/50.

XX DR P-PSDB: AAK45247.

XX New p53 related human gene p51, useful for diagnosis, investigation and

PT treatment of cancers and screening for potential cell proliferation

PT agents -

XX Example 1: Page 154-156; 163pp; Japanese.

XX The present sequence represents a human p51 gene, which is related to

CC p53 and has cell proliferation regulation and tumour suppression

CC activity. The p51 gene can be used in the investigation, diagnosis and

CC treatment of diseases such as cancer, with which the p53 family cell

CC proliferation regulation is associated. The p51 protein may be used for

CC screening potential agonists and antagonists of its regulatory function,

CC for use as drugs.

XX Sequence 2270 BP; 595 A; 677 C; 500 G; 498 T; 0 other;

Query Match 48.9%; Score 1376; DB 20; Length 2270;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctgtgataccaagaagcttgaagaaatgaatttgaacttcaagtggtgccacct 60  
|||||  
Db 1 tctgtgataccaagaagcttgaagaaatgaatttgaacttcaagtggtgccacct 60  
Oy 61 acagtaactgacctgacctataccagcgcttctgtaagaacccaagctcatctcttgg 120  
|||||  
Db 61 acagtaactgacctgacctataccagcgcttctgtaagaacccaagctcatctcttgg 120  
Oy 121 aaagaagaattatcagatccacatctgtccagagcacacagaacaatgaattcttcagt 180  
|||||  
Db 121 aaagaagaattatcagatccacatctgtccagagcacacagaacaatgaattcttcagt 180  
Oy 181 ccaagagtttcccaagcatatctgagatcttctggaacagccatattgttcaattcagccc 240  
|||||  
Db 181 ccaagagtttcccaagcatatctgagatcttctggaacagccatattgttcaattcagccc 240  
Oy 241 attgacttgaacttctgtgataaccatcagaagaatggtgcgaacaacaagaattgagatt 300  
|||||  
Db 241 attgacttgaacttctgtgataaccatcagaagaatggtgcgaacaacaagaattgagatt 300  
Oy 301 agcatggaactgtatccgatcagatcagactcagactcagactcagactcagactcagactc 360  
|||||  
Db 301 agcatggaactgtatccgatcagatcagactcagactcagactcagactcagactcagactc 360  
Oy 361 acgaacctgggctctctgtacacagacatgacacagatccaacagcctcgtccacc 420  
|||||  
Db 361 acgaacctgggctctctgtacacagacatgacacagatccaacagcctcgtccacc 420  
Oy 421 agtccctataacacagacacacagcagacagcgtcagcgccctgcgcctacgacag 480  
|||||  
Db 421 agtccctataacacagacacacagcagacagcgtcagcgccctgcgcctacgacag 480  
Oy 481 cccaagctccacttgaatgtctctctcattacacccgcatccctcccaacccagactac 540  
|||||  
Db 481 cccaagctccacttgaatgtctctctcattacacccgcatccctcccaacccagactac 540  
Oy 541 ccaagcccgcaagcttgcagctgtccttcacagcagctcagacccgcaagctcgccacc 600  
|||||  
Db 541 ccaagcccgcaagcttgcagctgtccttcacagcagctcagacccgcaagctcgccacc 600  
Oy 601 tggacgtattccactgaacttgaagaactctactgcacaattgcaagaagcatgcccacatc 660  
|||||  
Db 601 tggacgtattccactgaacttgaagaactctactgcacaattgcaagaagcatgcccacatc 660  
Oy 661 cagatcaaggtgataccccaccctcctcagggagctgttatccgcgcacatgctcttacc 720  
|||||  
Db 661 cagatcaaggtgataccccaccctcctcagggagctgttatccgcgcacatgctcttacc 720  
Oy 721 aaaaaagctgagcagctcagcagaggtgtgtgaagcggtgcccacaacatgagctgagccgt 780  
|||||  
Db 721 aaaaaagctgagcagctcagcagaggtgtgtgaagcggtgcccacaacatgagctgagccgt 780  
Oy 781 gatttcaacgagagacagatttgcctcctactgatttgaatcgtatgtagagggagacagc 840  
|||||  
Db 781 gatttcaacgagagacagatttgcctcctactgatttgaatcgtatgtagagggagacagc 840  
Oy 841 catgcccaagtatgtagaagatcccatcacaagaagaacagagtgctgtgtacctatgag 900  
|||||  
Db 841 catgcccaagtatgtagaagatcccatcacaagaagaacagagtgctgtgtacctatgag 900  
Oy 901 ccaccccggttgagcagtaattcaccagcagctgtgtacaattcatgtgtacaagcagct 960  
|||||  
Db 901 ccaccccggttgagcagtaattcaccagcagctgtgtacaattcatgtgtacaagcagct 960  
Oy 961 tgtgttgagaggtgaacccgcctccaatttaactatgttactctggaacccagagat 1020  
|||||  
Db 961 tgtgttgagaggtgaacccgcctccaatttaactatgttactctggaacccagagat 1020



Db 901 cccccccggtgtgacacgaattcagacagctctgttacaatttcatgtgtacagcagt 960  
Qy 961 tctgttgagagatgaataacgcgcctcccaatttaattcatctgttactctggaacagagat 1020  
Db 961 tctgttgagagatgaataacgcgcctcccaatttaattcatctgttactctggaacagagat 1020  
Qy 1021 gggcaagccctgggcccgcgcgtctgtttagagcccgagatctgtcttggcccaagaagac 1080  
Db 1021 gggcaagccctgggcccgcgcgtctgtttagagcccgagatctgtcttggcccaagaagac 1080  
Qy 1081 aggaagcgcgtatgaagatagcatcagaaagcagcaagtttcggacagtcacaagaacggt 1140  
Db 1081 aggaagcgcgtatgaagatagcatcagaaagcagcaagtttcggacagtcacaagaacggt 1140  
Qy 1141 gatgttagaagagccgcttctgtttagaacaacacatggtatccaaatgacatccatcaag 1200  
Db 1141 gatgttagaagagccgcttctgtttagaacaacacatggtatccaaatgacatccatcaag 1200  
Qy 1201 aaacgaagatcccccagatgatatgaactgtatacttaccagtgaggggccgtgagacttat 1260  
Db 1201 aaacgaagatcccccagatgatatgaactgtatacttaccagtgaggggccgtgagacttat 1260  
Qy 1261 gaatgtctgttgaagatcaagaagctccctggaactcatgtacgtacatcccttcacagaca 1320  
Db 1261 gaatgtctgttgaagatcaagaagctccctggaactcatgtacgtacatcccttcacagaca 1320  
Qy 1321 attgaaagctacagcagcaacagcagcagcagcagcagcagcagcagcagcagcagcagc 1376  
Db 1321 attgaaagctacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1376

RESULT 5

AAZ43913  
ID AAZ43913 standard; CDNA: 4846 BP.

AAZ43913:

14-MAR-2000 (first entry)

Human KET cDNA.

KET: anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;  
KW p53 family; angiogenic; cytotoxic; cancer; human; ss.

OS Homo sapiens.

PN W09961610-A2.

PD 02-DEC-1999.

PE 25-MAY-1999; 99WO-DE01557.

PR 25-MAY-1998; 98DE-1022985.

PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGENWANDTEN.

PI Paul D, Augustin M, Schmale H, Bamberger C;

DR WPI: 2000-062710/05.

DR P-PSDB: AAY50997.

PT New KET-encoding nucleic acid and related proteins, for diagnosis and

PT treatment of tumors

PS Claim 3; Page 23-26; 28pp; German.

CC This invention describes a novel KET-encoding nucleic acid (I) and its  
CC fragments, variants and mutants which has anticancer activity. (I)  
CC encodes a protein, (II), involved in control of the cell cycle and  
CC apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the  
CC p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to  
CC detect (I) in biological samples, specifically angiogenic tumor tissue,

CC including (I) sequences that have a homozygotic deletion and (b) to  
CC detect presence or absence of human chromosome 3q27 or murine chromosome  
CC 16, or their fragments, by hybridization. Also, (I) is used as a tumor  
CC suppressor, particularly in tumors where an alteration in the wild-type  
CC p53 allele has not been identified. (I) and (II) may also be used for  
CC development of specific cytotoxic agents and for predicting the risk of  
CC developing cancer. This sequence represents the human KET cDNA sequence  
CC described in the method of the invention.

XX Sequence 4846 BP; 1372 A; 1077 C; 990 G; 1406 T; 1 other;

Query Match 48.4%; Score 1364; DB 21; Length 4846;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1375; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 cgttataatcaagaacagttgaagaatgaatttgaacttcacggtgtgccacta 61  
Db 1 cgttataatcaagaacagttgaagaatgaatttgaacttcacggtgtgccacta 60  
Qy 62 cagtactgcccggacccttaccacagcggttcgtagaaa-cccagctcatttccttgg 120  
Db 61 cagtactgcccggacccttaccacagcggttcgtagaaa-cccagctcatttccttgg 120  
Qy 121 aaagaagttattacagatccacatgtccagagcacacagacaatgaattcctcagt 180  
Db 121 aaagaagttattacagatccacatgtccagagcacacagacaatgaattcctcagt 180  
Qy 181 ccagaggtttccacagatatacttgcgatttcttgcgaacagcctatagtcaagccc 240  
Db 181 ccagaggtttccacagatatacttgcgatttcttgcgaacagcctatagtcaagccc 240  
Qy 241 attgactgaactttgttgatgaacatcagaagaatgtgtgagacaacaagaattagatt 300  
Db 241 attgactgaactttgttgatgaacatcagaagaatgtgtgagacaacaagaattagatt 300  
Qy 301 agcatgagactgtatccgcacgtcagagactcgaccctgagtgaccatgttgccacagatc 360  
Db 301 agcatgagactgtatccgcacgtcagagactcgaccctgagtgaccatgttgccacagatc 360  
Qy 361 acgaaccttggggctccttgaaacagcatggaacagcagatcagaacggtcctctgcacc 420  
Db 361 acgaaccttggggctccttgaaacagcatggaacagcagatcagaacggtcctctgcacc 420  
Qy 421 agtccctataacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 480  
Db 421 agtccctataacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 480  
Qy 481 ccagctccacttcgattgtctctctccatcacccgcgcctccctccacaacagactac 540  
Db 481 ccagctccacttcgattgtctctctccatcacccgcgcctccctccacaacagactac 540  
Qy 541 ccaagcccgacagtttcgacgtgtctctccagcagtcgagcagccgccaagtccgaccac 600  
Db 541 ccaagcccgacagtttcgacgtgtctctccagcagtcgagcagccgccaagtccgaccac 600  
Qy 601 tggacgtattccactggaactgaagaactctacttccaaatgcaagaagacccccatc 660  
Db 601 tggacgtattccactggaactgaagaactctacttccaaatgcaagaagacccccatc 660  
Qy 661 cagatcaaggtgatgaccccaactcctcagaggagtggtatccgcgcacatgctgtctac 720  
Db 661 cagatcaaggtgatgaccccaactcctcagaggagtggtatccgcgcacatgctgtctac 720  
Qy 721 aaaaagctgagcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780  
Db 721 aaaaagctgagcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780  
Qy 781 gattccaagagagcagattgcccctcctagctatcttgcagtgtagagggaggaacgc 840  
Db 781 gattccaagagagcagattgcccctcctagctatcttgcagtgtagagggaggaacgc 840  
Qy 841 catgccagtagtagaagatcccatcacagaagacagagtgctgtgtacctaagag 900

|||||  
Db 841 catgccagatgtatgaagatccatccatcaagaaagacagatgtgtctgtactatgag 900  
Oy 901 ccacccaggttgtagctgaattcaacagacagtcgttacaattcatgttgaacagcag 960  
Db 901 cccccccaggttgtagctgaattcaacagacagtcgttacaattcatgttgaacagcag 960  
Oy 961 tgtgttgtaggagatgaacccgctcccaatttaactatgttactctgtgaacccagat 1020  
Db 961 tgtgttgtaggagatgaacccgctcccaatttaactatgttactctgtgaacccagat 1020  
Oy 1021 gggcaagtccttgagccgagcagtcgtcttgagcccgagatctgtctgcccaggaagac 1080  
Db 1021 gggcaagtccttgagccgagcagtcgtcttgagcccgagatctgtctgcccaggaagac 1080  
Oy 1081 aggaagcgagatgaagatagatcgtcagaagcagcagatgttggaagatgacaagacgt 1140  
Db 1081 aggaagcgagatgaagatagatcgtcagaagcagcagatgttggaagatgacaagacgt 1140  
Oy 1141 gatgtacgaagcgccgcttctcgcagaaacacatggtatccagatgacatccatcaag 1200  
Db 1141 gatgtacgaagcgccgcttctcgcagaaacacatggtatccagatgacatccatcaag 1200  
Oy 1201 aaacgaagatcccccagatgatgaactgttatacttaccagtgagggcggtgagacttat 1260  
Db 1201 aaacgaagatcccccagatgatgaactgttatacttaccagtgagggcggtgagacttat 1260  
Oy 1261 gaaatgctgttgaagatacaaaagtcctctggaactcatgacgtactcctctcagacaca 1320  
Db 1261 gaaatgctgttgaagatacaaaagtcctctggaactcatgacgtactcctctcagacaca 1320  
Oy 1321 atggaacgtacaggaacagcaacagcagcagcagcagcagcagcagcagcagcagcagc 1376  
Db 1321 atggaacgtacaggaacagcaacagcagcagcagcagcagcagcagcagcagcagcagc 1376

RESULT 6  
AAC66031  
ID AAC66031 standard; CDNA; 4849 BP.

AC AAC66031;

DT 21-FEB-2001 (first entry)

DE Human Lung cancer-associated CDNA p63 isoform 5.

KM Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
KW vaccine; detection; ss.

OS Homo sapiens.

PN WO200061612-A2.

PD 19-OCT-2000.

PF 03-APR-2000; 2000WO-US08896.

PR 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

PA (CORI-) CORIXA CORP.

PI Wang T, Fan L;

DR MPI: 2000-62839/60.

DR P-PSDB; AAB11361.

PT Isolated polypeptide comprising an immunogenic portion of a lung tumor  
PT protein is used for detecting and monitoring progression of lung cancer  
PT in a patient -

XX  
PS Claim 25a: Page 240-242; 261pp; English.  
CC This invention describes a novel isolated polypeptide (I) which  
XX comprising an immunogenic portion of a lung tumor protein or variant (P2)  
CC which have cytostatic activity. The polypeptides and polynucleotides are  
CC used in compositions and vaccines to inhibit the development of cancer,  
CC especially lung cancer. In a patient. Methods described in the invention  
CC can be used to monitor the progression of a cancer by carrying out the  
CC detection at subsequent time points and comparing the results from the  
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient  
CC are treated with P2, polynucleotides encoding P2 or antigen presenting  
CC cells expressing P2 and then administered to the patient to inhibit  
CC development of cancer.  
XX  
SQ Sequence 4849 BP; 1377 A; 1076 C; 988 G; 1407 T; 1 other;

Query Match 48.4%; Score 1364; DB 21; Length 4849;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1375; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 2 cgttgatcaagaacagctgaaggaatgaatttgaactcaaggtgtgcaccccta 61  
Db 1 cgttgatcaagaacagctgaaggaatgaatttgaactcaaggtgtgcaccccta 60  
Oy 62 cagtagtccttgacccttaacatccagcgttctgtagaa-ccagctcatctcttgg 120  
Db 61 cagtagtccttgacccttaacatccagcgttctgtagaa-ccagctcatctcttgg 120  
Oy 121 aaagaagatattacagatccacatgctccagagcacacagacaatgaattcctcagt 180  
Db 121 aaagaagatattacagatccacatgctccagagcacacagacaatgaattcctcagt 180  
Oy 181 ccagaggtttccagacatctggatcttctggaacagcctatagtctcaagccc 240  
Db 181 ccagaggtttccagacatctggatcttctggaacagcctatagtctcaagccc 240  
Oy 241 attgactggaactgtgtgagaaacatcagaaggtgtgagacaagaatgtgaatt 300  
Db 241 attgactggaactgtgtgagaaacatcagaaggtgtgagacaagaatgtgaatt 300  
Oy 301 agcatggaactgtatccgagatcagagactcagacactgaatgaccccatgtgcccagatc 360  
Db 301 agcatggaactgtatccgagatcagagactcagacactgaatgaccccatgtgcccagatc 360  
Oy 361 acgaacctggggctcctgaacagcatggaacagcagatcagaagcgtcctctgcacc 420  
Db 361 acgaacctggggctcctgaacagcatggaacagcagatcagaagcgtcctctgcacc 420  
Oy 421 agtccctataacagacacagcgcagagacagcgtcagcgccctcgccctcagcagag 480  
Db 421 agtccctataacagacacagcgcagagacagcgtcagcgccctcgccctcagcagag 480  
Oy 481 ccagatccacacttgatgtctctctccatcaaccgcgcacatccctccaacacagcagatc 540  
Db 481 ccagatccacacttgatgtctctctccatcaaccgcgcacatccctccaacacagcagatc 540  
Oy 541 ccagcccgacagatctgacagtgctctcctcagcagcgtcgaagacgcgaatcggcacc 600  
Db 541 ccagcccgacagatctgacagtgctctcctcagcagcgtcgaagacgcgaatcggcacc 600  
Oy 601 tggacgtatccactgaactgaagaaactctactgccaatttgaagaagacatgcccatac 660  
Db 601 tggacgtatccactgaactgaagaaactctactgccaatttgaagaagacatgcccatac 660  
Oy 661 cagatcaagtgatgatacccccactcctcagggagctgttatccgcgcatcctgtctac 720  
Db 661 cagatcaagtgatgatacccccactcctcagggagctgttatccgcgcatcctgtctac 720  
Oy 721 aaaaaagctgagcagctcagcaggaagtgtgtagcggtgtcccaacatgagcagcgt 780  
Db 721 aaaaaagctgagcagctcagcaggaagtgtgtagcggtgtcccaacatgagcagcgt 780



```

OY 761 gaattcaacagagagacagattgccccctctactgattgattcaggtagagggaacagc 840
DB 761 gaattcaacagagagacagattgccccctctactgattgattcaggtagagggaacagc 840
OY 841 catgcccagatgtatgaagatcccatcacaggaagacagagtgctgttaccattatgag 900
DB 841 catgcccagatgtatgaagatcccatcacaggaagacagagtgctgttaccattatgag 900
OY 901 ccacccaggttgcagctgaattcaacagagctctgtacaatttcattgttaacagcagt 960
DB 901 ccacccaggttgcagctgaattcaacagagctctgtacaatttcattgttaacagcagt 960
OY 961 tctgttgagagatgaacagccgcttccatcttaattcattgttacccttgaaacccagagt 1020
DB 961 tctgttgagagatgaacagccgcttccatcttaattcattgttacccttgaaacccagagt 1020
OY 1021 gggcagatccttggcgccagcgtctgtttgagcccgagatctgtcttgcacaggaagagac 1080
DB 1021 gggcagatccttggcgccagcgtctgtttgagcccgagatctgtcttgcacaggaagagac 1080
OY 1081 aggaagcgcggtatgaagatagcttcagaaagcagcaagtttcggacagttacaagaacaggt 1140
DB 1081 aggaagcgcggtatgaagatagcttcagaaagcagcaagtttcggacagttacaagaacaggt 1140
OY 1141 gatgtacgaagcgcgcttctctacagacacacatgttatccagatgacatccatcaag 1200
DB 1141 gatgtacgaagcgcgcttctctacagacacacatgttatccagatgacatccatcaag 1200
OY 1201 aaacgaagatcccccagatgatgaactgttatcttaccagtgagggcgctgagacttat 1260
DB 1201 aaacgaagatcccccagatgatgaactgttatcttaccagtgagggcgctgagacttat 1260
OY 1261 gaaatgcctgttgaagaataaagaagctccctgtgaactcattgcagctacccttcctcagacaca 1320
DB 1261 gaaatgcctgttgaagaataaagaagctccctgtgaactcattgcagctacccttcctcagacaca 1320
OY 1321 attgaacgtacagcagcaacagcaagcagcagcagcacttacttcagaaaca 1376
DB 1321 attgaacgtacagcagcaacagcaagcagcagcagcacttacttcagaaaca 1376

RESULT 7
AAK58574
ID AAK58574 standard; cDNA: 1347 BP.
XX
AC AAK58574;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cell regulatory protein p63, isoform hTAp63 gamma, cDNA.
XX
KW Cell regulatory protein; p63; hTAp63 gamma; TAp63 gamma; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT misc_difference 1254
FT /*tag" a
FT /*note" "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to maintain
FT the nucleotide numbering given in the
FT specification for this sequence"
PN M09919357-A2.
XX
PD 22-APR-1999.
XX
PF 02-OCT-1998; 98WO-US21992.
XX

```

```

PR 29-MAY-1998; 98US-0087216.
PR 15-OCT-1997; 97US-0062076.
PA (HARD ) HARVARD COLLEGE.
XX
PI McKeon F, Yang A;
XX
DR WPI: 1999-277595/23.
DR P-PSDB; AAK05955.
XX
PT New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
PS Claim 1; Fig 11; 161pp; English.
XX
CC The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as delta1 and TA forms, where the delta1 form lacks the
CC transactivation domain. The present sequence represents a cDNA
CC clone encoding human TAp63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta1 isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AA05053-64), polynucleotides (see
CC AAK58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 1347 BP; 374 A; 381 C; 316 G; 275 T; 1 other.

Query Match 47.8%; Score 1346; DB 20; Length 1347;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 145 atgtcccgagagacacagacaatgaattccctcagttccagagagtttcacagatatcgg 204
DB 1 atgtcccgagagacacagacaatgaattccctcagttccagagagtttcacagatatcgg 60
OY 205 gatttcttggaaacagcctatatgttccagttcagcccatgagttgaactttgtgatga 264
DB 61 gatttcttggaaacagcctatatgttccagttcagcccatgagttgaactttgtgatga 120
OY 265 ccatcagaagaatgtgtgcagacaagaattgagattagatgagatgcagatgcag 324
DB 121 ccatcagaagaatgtgtgcagacaagaattgagattagatgagatgcagatgcag 180
OY 325 gactcgtgacctgtgaccccatgtgcccacagttacacgaaccttgggtcctgcagc 384
DB 161 gactcgtgacctgtgaccccatgtgcccacagttacacgaaccttgggtcctgcagc 240
OY 385 atgacacagcagatcagaagcgcctcgtccacagttccctataacaacaagaacgcg 444
DB 241 atgacacagcagatcagaagcgcctcgtccacagttccctataacaacaagaacgcg 300
OY 445 cagaacagcgttcacggcgccctcgtccctacagcagccagctccacttcgattgtctc 504

```

```
Dh 301 cagaacagcgtcaagcgccctcgccctacgacagcccagctccaccttcgtctc 360
Oy 505 tctccatcacccgcacatccctcccaaacgcgtaccacgcccagcttcgacgtg 564
Dh 361 tctccatcacccgcacatccctcccaaacgcgtaccacgcccagcttcgacgtg 420
Oy 565 tctctccagcagtcgagacagcccaagtcgacgttcgacgttcacgttaactgaag 624
Dh 421 tctctccagcagtcgagacagcccaagtcgacgttcgacgttcacgttaactgaag 480
Oy 625 aaactctactgcgaatttgcaagaacatgcccacccacgttaagaagtgtgacccact 684
Dh 481 aaactctactgcgaatttgcaagaacatgcccacccacgttaagaagtgtgacccact 540
Oy 685 cctcagggagcgttatacccgcccatgcccgtctcctcaaaaaagcggagacgtcagag 744
Dh 541 cctcagggagcgttatacccgcccatgcccgtctcctcaaaaaagcggagacgtcagag 600
Oy 745 gtgtgtgaagcggatgcccacacatgagctgagcgttgaaatcaacgagggagacagatg 804
Dh 601 gtgtgtgaagcggatgcccacacatgagctgagcgttgaaatcaacgagggagacagatg 660
Oy 805 cctctatgcatcttgatcttgagtaagggggaacagccatgcccagatgtaagaatccc 864
Dh 661 cctctatgcatcttgatcttgagtaagggggaacagccatgcccagatgtaagaatccc 720
Oy 865 atcacagagagacagagtgctgtgtgtacctaagccacccaggttgacgttaattc 924
Dh 721 atcacagagagacagagtgctgtgtgtacctaagccacccaggttgacgttaattc 780
Oy 925 acgacagctctgtacaatttcagtgtacacagcagctgtgtgtgagggagatgaacgcgt 984
Dh 781 acgacagctctgtacaatttcagtgtgtacacagcagctgtgtgtgagggagatgaacgcgt 840
Oy 985 ccaatttataatcattgttactcttgaaaccagagatgagcgaagtcctggccgacgcgtgc 1044
Dh 841 ccaatttataatcattgttactcttgaaaccagagatgagcgaagtcctggccgacgcgtgc 900
Oy 1045 ttgtgagcccgagatctgtctgtcccaagaagaagcgaagggcgatgaagaatgacatc 1104
Dh 901 ttgtgagcccgagatctgtctgtcccaagaagaagcgaagggcgatgaagaatgacatc 960
Oy 1105 agaaagcagcgaagttcggacagtaacaagaacggtgagtgtacgaagcgcgtttcgt 1164
Dh 961 agaaagcagcgaagttcggacagtaacaagaacggtgagtgtacgaagcgcgtttcgt 1020
Oy 1165 cagaacacacagtgatccagatgacatccatcaagaagaacgagatccccaatgatgaa 1224
Dh 1021 cagaacacacagtgatccagatgacatccatcaagaagaacgagatccccaatgatgaa 1080
Oy 1225 cgttatacttaccagtgagggcgctgagactttaagaatgctttgaaagtaacaag 1284
Dh 1081 cgttatacttaccagtgagggcgctgagactttaagaatgctttgaaagtaacaag 1140
Oy 1285 tccctggaactatgacgtaccttccctcagcacacaatgaaacgtacaggaacaagcaa 1344
Dh 1141 tccctggaactatgacgtaccttccctcagcacacaatgaaacgtacaggaacaagcaa 1200
Oy 1345 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1404
Dh 1201 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1260
Oy 1405 ctgtgtgagcccgagagagaacatcccaaaacatctgacgtcttcttagaatcccaag 1464
Dh 1261 ctgtgtgagcccgagagagaacatcccaaaacatctgacgtcttcttagaatcccaag 1320
Oy 1465 cccccaaacagatcagtgtaaccatag 1491
Dh 1321 cccccaaacagatcagtgtaaccatag 1347
```

RESULT 8  
AAx58573

```
ID ID AAx58573 standard; cDNA: 1551 BP.
XX AC AAx58573;
XX XX
Dh 16-AUG-1999 (first entry)
XX XX
Dh Human cell regulatory protein p63, isoform huTap63 beta, cDNA.
XX XX
Dh Cell regulatory protein: p63; huTap63 beta; TAp63 beta; human;
XX XX
Dh cancer; tumour suppressor; cell cycle control; apoptosis;
XX XX
Dh cell proliferation; cell differentiation; therapy; ss.
XX XX
Dh Homo sapiens.
XX XX
Dh W09919357-A2.
XX XX
Dh 22-APR-1999.
XX XX
Dh 02-OCT-1998; 98WO-US21992.
XX XX
Dh 29-MAY-1998; 98US-0087216.
XX XX
Dh 15-OCT-1997; 97US-0062076.
XX XX
Dh (HARD ) HARVARD COLLEGE.
XX XX
Dh McKeon F, Yang A;
XX XX
Dh WPI: 1999-277595/23.
XX XX
Dh P-PSDB: AAY05954.
XX XX
Dh New isolated p63 cell regulatory protein for, e.g. treatment of
XX XX
Dh tumours
XX XX
Dh Claim 1: Fig 10; 161pp; English.
XX XX
Dh The present invention concerns the discovery of a new family of
XX XX
Dh cell regulatory proteins (CRPs) termed the p63 family of proteins,
XX XX
Dh which demonstrate certain sequence identity to known tumour
XX XX
Dh suppressor proteins p53 and p73. It has been observed that the
XX XX
Dh intron-exon organisation is conserved between p73 and p53, and from
XX XX
Dh known exon and intron sizes for these 2 genes, it was possible to
XX XX
Dh identify new members of this gene family using a PCR-based strategy
XX XX
Dh of amplifying 2 exons in a conserved domain and their intervening
XX XX
Dh intron. The human p53 gene was localised to chromosomal position
XX XX
Dh 3q27-29. At least 6 different isoforms exist. Splice variants
XX XX
Dh differing at the C-terminus have been designated as alpha, beta and
XX XX
Dh gamma forms, while p63 members differing in the N-terminus are
XX XX
Dh designated as delta and TA forms, where the delta form lacks the
XX XX
Dh transactivation domain. The present sequence represents a cDNA
XX XX
Dh clone encoding human TAp63 beta. p63 was detected in a variety of
XX XX
Dh human and mouse tissue. It demonstrates remarkably divergent
XX XX
Dh activities, such as the ability to transactivate p53 reporter genes
XX XX
Dh and induce apoptosis. Cessation or down-regulation of p63 expression
XX XX
Dh may play a critical role in the process of cervical squamous
XX XX
Dh differentiation, both benign and neoplastic. Delta isoforms of p63
XX XX
Dh act as dominant negatives towards transactivation by p53 and p63.
XX XX
Dh p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
XX XX
Dh cachexia) and neuronal differentiation and related degenerative
XX XX
Dh disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
XX XX
Dh AAx58572-83) and anti-p63 antibodies of the invention can be used to
XX XX
Dh identify compounds useful for treating disorders involving such
XX XX
Dh processes, in detection and diagnosis, and in the production of
XX XX
Dh transgenic animals.
XX XX
Dh Sequence 1551 BP: 425 A; 466 C; 350 G; 310 T; 0 other;
XX XX
Dh
XX XX
Dh Query Match 43.8%; Score 1232; DB 20; Length 1551;
XX XX
Dh Best Local Similarity 100.0%; Pred. No. 0;
XX XX
Dh Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
Dh 145 atgtccagagacacagacaaatgattcctcagtcagaggtttccagcatatctcg 204
XX XX
```

```
Db 1 atgtccagagacacagacaatgaattctctcaagtttccagacatactcg 60
Oy 205 gattcttcggagacagcattatgttcaagccatttgattgaatttgatgaa 264
Db 61 gattcttcggagacagcattatgttcaagccatttgattgaatttgatgaa 120
Oy 265 ccatcagaagaatgtgtgcagacaagaatcgaatgaatgaatgaatgaatgaat 324
Db 121 ccatcagaagaatgtgtgcagacaagaatgaatgaatgaatgaatgaatgaat 180
Oy 325 gactcgaagctgtatgacccatgtgtgcacagtaacagctgtgtcctgaagc 384
Db 181 gactcgaagctgtatgacccatgtgtgcacagtaacagctgtgtcctgaagc 240
Oy 385 atggaaccagcagatcacaagcgtcctcgttcaccagttccataaacaagcagcg 444
Db 241 atggaaccagcagatcacaagcgtcctcgttcaccagttccataaacaagcagcg 300
Oy 445 cagaacacagtcacagcgccctcgtcctcagcagacagccacacttcagctctc 504
Db 301 cagaacacagtcacagcgccctcgtcctcagcagacagccacacttcagctctc 360
Oy 505 tctccatacccgccatccctccacaacagcagtaaccagcgccagatctcgagtg 564
Db 361 tctccatacccgccatccctccacaacagcagtaaccagcgccagatctcgagtg 420
Oy 565 tctccatacccgctgagacagcgccagcagcagcagcagcagcagcagcagcagc 624
Db 421 tctccatacccgctgagacagcgccagcagcagcagcagcagcagcagcagcagc 480
Oy 625 aaactctactgcacaatgtgcagaagacatgcaccatccagatcaagtgatgcaccact 684
Db 481 aaactctactgcacaatgtgcagaagacatgcaccatccagatcaagtgatgcaccact 540
Oy 685 cctcagagagctgtatctcgcgcagcagtcctgtctacaacaaagctgtgacagtcagcgag 744
Db 541 cctcagagagctgtatctcgcgcagcagtcctgtctacaacaaagctgtgacagtcagcgag 600
Oy 745 gtgtgtgaagcggtgtcccaacacatagctgagcagtgaaatcaagaaggaagattgccc 804
Db 601 gtgtgtgaagcggtgtcccaacacatagctgagcagtgaaatcaagaaggaagattgccc 660
Oy 805 cctcctagatctgtatctcgcgcagcagtcctgtctacaacaaagctgtgacagtcagcgag 864
Db 661 cctcctagatctgtatctcgcgcagcagtcctgtctacaacaaagctgtgacagtcagcgag 720
Oy 865 atcacagaagaacagagatgtgtcgtgtacactatgagccacccaggtgtgacatgaatcc 924
Db 721 atcacagaagaacagagatgtgtcgtgtacactatgagccacccaggtgtgacatgaatcc 780
Oy 925 acgacagctgtgtacaatttcaatgtgttaacagcagttgtgtggaggatgaacgcgctg 984
Db 781 acgacagctgtgtacaatttcaatgtgttaacagcagttgtgtggaggatgaacgcgctg 840
Oy 985 ccaatttcaatcatgttactctcgtgaaacacagagatgagcagtcctgtgacgcagcgtcg 1044
Db 841 ccaatttcaatcatgttactctcgtgaaacacagagatgagcagtcctgtgacgcagcgtcg 900
Oy 1045 ttgtgagcccgagatctgtgtcgtgtccaggaagaacagagagcgagatgaagaatgacatc 1104
Db 901 ttgtgagcccgagatctgtgtcgtgtccaggaagaacagagagcgagatgaagaatgacatc 960
Oy 1105 agaagagcgagcaggttctgagacagtcacaagaacggtgtatgtgtgacgaagcccggtttgt 1164
Db 961 agaagagcgagcaggttctgagacagtcacaagaacggtgtatgtgtgacgaagcccggtttgt 1020
Oy 1165 cagaacacacatgtgtatccagatccatccacaagaacgagaatccccaatgatgaa 1224
Db 1021 cagaacacacatgtgtatccagatccatccacaagaacgagaatccccaatgatgaa 1080
Oy 1225 ctgttatacttaacagtgagggcgctgtgagacttatgaatgctgttgaagaatcaagaag 1284
Db 1081 ctgttatacttaacagtgagggcgctgtgagacttatgaatgctgttgaagaatcaagaag 1140
```

```
Oy 1285 tccctggaactcatgtacgtactctcctcagcacacaattgaacgttacagcagaagca 1344
Db 1141 tccctggaactcatgtacgtactctcctcagcacacaattgaacgttacagcagaagca 1200
Oy 1345 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1376
Db 1201 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1232
```

## RESULT 9

AAC66033

ID AAC66033 standard; cDNA; 1551 BP.

XX AAC66033;

DT 21-FEB-2001 (first entry)

DE Human Lung cancer-associated cDNA p63 isoform 7.

KM Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;

KM vaccine; detection; ss.

OS Homo sapiens.

PN W0200061612-A2.

PD 19-OCT-2000.

PF 03-APR-2000; 2000WO-US08896.

PR 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 98US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.

PA Wang T, Fan L;

DR WPI; 2000-628399/60.

DR P-PSDB; AAB11363.

PT Isolated polypeptide comprising an immunogenic portion of a lung tumor

PT protein is used for detecting and monitoring progression of lung cancer

PT in a patient -

PS Claim 25a; Page 242-243; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which

XX comprising an immunogenic portion of a lung tumor protein or variant (P2)

XX which have cytostatic activity. The polypeptides and polynucleotides are

XX used in compositions and vaccines to inhibit the development of cancer,

XX especially lung cancer, in a patient. Methods described in the invention

XX can be used to monitor the progression of a cancer by carrying out the

XX detection at subsequent time points and comparing the results from the

XX different time points. CD4+ and/or CD8+ T-cells isolated from a patient

XX are treated with P2, polynucleotides encoding P2 or antigen presenting

XX cells expressing P2 and then administered to the patient to inhibit

XX development of cancer.

XX Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;

Query Match 43.8%; Score 1232; DB 21; Length 1551;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 145 atgtccagagcagacagacaatgaattcctcagtcagagaggtttccagacatactcg 204

Db 1 atgtccagagcagacagacaatgaattcctcagtcagagaggtttccagacatactcg 60

```

Oy 205 gattctcgaacagcctatatgttcagtcaagcccatgacctggaacttgtgataa 264
    |||||||
Db 61 gattctcgaacagcctatatgttcagtcaagcccatgacctggaacttgtgataa 120
Oy 265 ccatcagaagatggtgcgacaacaagatgagattagcatgagctgtatccgcattcag 324
    |||||||
Db 121 ccatcagaagatggtgcgacaacaagatgagattagcatgagctgtatccgcattcag 180
Oy 325 gactcgagcctgtagcccccattgtgccaagttacaggaacctgtggtcctcgaacac 384
    |||||||
Db 181 gactcgagcctgtagcccccattgtgccaagttacaggaacctgtggtcctcgaacac 240
Oy 385 atggaccagcagattcagaacggtctcctcgtccaccagtcctcattacaacacagcagcg 444
    |||||||
Db 241 atggaccagcagattcagaacggtctcctcgtccaccagtcctcattacaacacagcagcg 300
Oy 445 cagaagaagctcagcgccctcgcctcagcagacagccagctccacttcgatgctc 504
    |||||||
Db 301 cagaagaagctcagcgccctcgcctcagcagacagccagctccacttcgatgctc 360
Oy 505 tctcaccacccgcctcctccccaacacagcagctaccagcgcccgacagtttcgacgtg 564
    |||||||
Db 361 tctcaccacccgcctcctccccaacacagcagctaccagcgcccgacagtttcgacgtg 420
Oy 565 tcccttcagcagtcgagcaccgccaagtcgcgcaccctggacgctatccactgaactgaag 624
    |||||||
Db 421 tcccttcagcagtcgagcaccgccaagtcgcgcaccctggacgctatccactgaactgaag 480
Oy 625 aaactctactgcgaattgcgaagacatgcccatccatacaaggtgtgtgacccacct 684
    |||||||
Db 481 aaactctactgcgaattgcgaagacatgcccatccatacaaggtgtgtgacccacct 540
Oy 685 cctcagggagcgtgtatcctgcgcacatgctgtctacaaaagcctgagacgtcagcgag 744
    |||||||
Db 541 cctcagggagcgtgtatcctgcgcacatgctgtctacaaaagcctgagacgtcagcgag 600
Oy 745 gtagtggaagcgtgtgcccccaacatgagcgtgagccgttgatcaacagaggacagattg 804
    |||||||
Db 601 gtagtggaagcgtgtgcccccaacatgagcgtgagccgttgatcaacagaggacagattg 660
Oy 805 cctcctcagtcattgtatgtagtagaggggaacacagcagctatgtagaataccc 864
    |||||||
Db 661 cctcctcagtcattgtatgtagtagaggggaacacagcagctatgtagaataccc 720
Oy 865 atcacaggaagacagagtgctgtgtacctaatagcaacccaggttggcacgtgaatc 924
    |||||||
Db 721 atcacaggaagacagagtgctgtgtacctaatagcaacccaggttggcacgtgaatc 780
Oy 925 acgacagctgtgtacaaattcattgtgtacagcagttgtgtggaggatgataccgcgtg 984
    |||||||
Db 781 acgacagctgtgtacaaattcattgtgtacagcagttgtgtggaggatgataccgcgtg 840
Oy 985 ccaatttaataatcattgtgtactctcgaacacagagatgggcaagtcctctggccgacgtgc 1044
    |||||||
Db 841 ccaatttaataatcattgtgtactctcgaacacagagatgggcaagtcctctggccgacgtgc 900
Oy 1045 tttagggcccgagatctgtgtgtgcccaggaagagacaggaaggcgatgagaatgacatc 1104
    |||||||
Db 901 tttagggcccgagatctgtgtgtgcccaggaagagacaggaaggcgatgagaatgacatc 960
Oy 1105 agaaagcagcaggttcggacagatcaagaagcgtgtgtgtgacgaacacgcccgtttgt 1164
    |||||||
Db 961 agaaagcagcaggttcggacagatcaagaagcgtgtgtgtgacgaacacgcccgtttgt 1020
Oy 1165 cagaacacacatgatacctcagatgacatcacaagaacgaagatcccccagatgtgaa 1224
    |||||||
Db 1021 cagaacacacatgatacctcagatgacatcacaagaacgaagatcccccagatgtgaa 1080
Oy 1225 ctgtatattacacagtgtaggggcccgtgtgagacttatgaaatgctgttgaagatcaagaag 1284
    |||||||
Db 1081 ctgtatattacacagtgtaggggcccgtgtgagacttatgaaatgctgttgaagatcaagaag 1140
Oy 1285 tccctggaactcatgtagtacctctcctcagcacacaattggaagctacagcgaacagcaa 1344

```

```

Db 1141 tccctggaactcatgtagtacctctcctcagcacacaattgtaacgtacagcgaacagaa 1200
Oy 1345 cagcagcagcaccagcacttactcagaaca 1376
    |||||||
Db 1201 cagcagcagcaccagcacttactcagaaca 1232

RESULT 10
AA58572
ID AA58572 standard; cDNA; 1926 BP.
XX
XX
AC AA58572;
XX
XX 16-AUG-1999 (first entry)
DT
XX
XX Human cell regulatory protein p63, isoform hupap63 alpha, cDNA.
DE
XX
XX Cell regulatory protein; p63; hupap63 alpha; TP63 alpha; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy; ss.
XX
OS Homo sapiens.
XX
XX W09919357-A2.
XX
XX 22-APR-1999.
XX
XX 02-OCT-1998; 98WO-US21992.
XX
XX 29-MAY-1998; 98US-0087216.
XX
XX 15-OCT-1997; 97US-0062076.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX McKeon F, Yang A;
XX
XX WPI; 1999-277595/23.
XX
XX P-PSDB; AAY05953.
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
XX tumours
XX
XX Claim 1; Fig 9; 161pp; English.
XX
XX The present invention concerns the discovery of a new family of
XX cell regulatory proteins (CRPs) termed the p63 family of proteins,
XX which demonstrate certain sequence identity to known tumour
XX suppressor proteins p53 and p73. It has been observed that the
XX intron-exon organisation is conserved between p73 and p53, and from
XX known exon and intron sizes for these 2 genes, it was possible to
XX identify new members of this gene family using a PCR-based strategy
XX of amplifying 2 exons in a conserved domain and their intervening
XX intron. The human p53 gene was localised to chromosomal position
XX 3q27-29. At least 6 different isoforms exist. Splice variants
XX differing at the C-terminus have been designated as alpha, beta and
XX gamma forms, while p63 members differing in the N-terminus are
XX designated as delta1 and TA forms, where the delta1 form lacks the
XX transactivation domain. The present sequence represents a cDNA
XX clone encoding human TP63 alpha. p63 was detected in a variety of
XX human and mouse tissue. It demonstrates remarkably divergent
XX activities, such as the ability to transactivate p53 reporter genes
XX and induce apoptosis. Cessation or down-regulation of p63 expression
XX may play a critical role in the process of cervical squamous
XX differentiation, both benign and neoplastic. Delta1 isoforms of p63
XX act as dominant negatives towards transactivation by p53 and p63.
XX p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
XX cachexia) and neuronal differentiation and related degenerative
XX disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
XX AA58572-83) and anti-p63 antibodies of the invention can be used to
XX identify compounds useful for treating disorders involving such
XX processes, in detection and diagnosis, and in the production of
XX transgenic animals.

```



CC The present invention concerns the discovery of a new family of  
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,  
CC which demonstrate certain sequence identity to known tumour  
CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using  
CC RACE. Sequencing of the amplification product indicated that the  
CC amplified cDNA possessed a truncated N-terminus, i.e. the  
CC transactivation domain was absent. Additional splice variants were  
CC identified by screening a cDNA library with a probe corresponding  
CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice  
CC variants differing at the C-terminus are designated as alpha, beta  
CC and gamma forms, while p63 members differing in the N-terminus are  
CC designated as delta1 and TA forms, where the delta1 form lacks the  
CC transactivation domain. The present sequence represents a cDNA  
CC clone encoding mouse TAp63 gamma. p63 was detected in a variety of  
CC human and mouse tissue. It demonstrates remarkably divergent  
CC activities, such as the ability to transactivate p53 reporter genes  
CC and induce apoptosis. Cessation or down-regulation of p63 expression  
CC may play a critical role in the process of cervical squamous  
CC differentiation, both benign and neoplastic. Delta1 isoforms of p63  
CC act as dominant negatives towards transactivation by p53 and p63.  
CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.  
CC cachexia) and neuronal differentiation and related degenerative  
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see  
CC AAX8572-83) and anti-p63 antibodies of the invention can be used to  
CC identify compounds useful for treating disorders involving such  
CC processes, in detection and diagnosis, and in the production of  
CC transgenic animals.

CC Sequence 1452 BP; 394 A; 425 C; 341 G; 289 T; 3 other:

Query Match 43.3% Score 1218.2; DB 20; Length 1452;  
Best Local Similarity 90.5% Pred. No. 0;  
Matches 1325; Conservative 0; Mismatches 126; Indels 13; Gaps 2;

QY 29 atgaatttgaacttcacggtgtgacccctacagtagtgcctgcagcccttaactcag 88  
DB 1 atgaatttgaacttcacggtgtgacccctacagtagtgcctgcagcccttaactcag 60  
QY 89 cgttcgttagaaa-ccagatcatcttctcttgaaagaagtattatccagccacatg 147  
DB 61 cgttcattagaacccacagctcatcttcgtgaaagaagtattatccagctcagctg 120  
QY 148 tcccgagagacacagacaagaatgaattcctcagtcagagagtttccagacatctggat 207  
DB 121 tccgagagacacacagacaagaatgaattcctcagtcagagagtttccagacatctggat 180  
QY 208 ttctctgaaacagcctatatgttcagttcagcccatgtgacttgaaattgttgataaaca 267  
DB 181 ttctctgaaacagcctatatgttcagttcagcccatgtgacttgaaattgttgataaaca 240  
QY 268 tcaagaagatgtgacgaacaagaattgagattagatgagatgacgtatccgacatgagac 327  
DB 241 tccgaaatgtgacgaacaagaattgagattagatgagatgacgtatccgacatgagac 300  
QY 328 tccgagccctgagtgaccctatgtgacgaagatgacgaagacccctgctcctgaacagatg 387  
DB 301 tccagaccctgagtgaccctatgtgacgaagatgacgaagacccctgctcctgaacagatg 360  
QY 388 gaccagcagatcagaagcgtcctcgtccacccagttcccttaacaagacagacagcag 447  
DB 361 gaccagcagatcagaagcgtcctcgtccacccagttcccttaacaagacagacagcag 420  
QY 448 aacagcgtcagcgcgcctcgtcctcagacagccagcctccacctcgtatctctct 507  
DB 421 aatagcgtgacgycgcctcgtcctcagacagccagcctccacctcgtatctctctct 480  
QY 508 ccataccgcgcacccctcccaacacgactaccagcccgacagcttgaagctcctcc 567  
DB 481 ccatccctcgtcactcctcccaacacgactaccagcccgacagcttgaagctcctcc 540  
QY 568 ttccagcagtcagacacccagctcgcacccctgagcgttccacgtgaactgaagaagaa 627  
DB 541 ttccagcagtcagacacccagctcgcacccctgagcgttccacgtgaactgaagaagaa 600  
QY 628 ctctactgcaaatctgcaagacatgcccacatccagatcaagctgataccaccctct 687  
DB 601 cgttactgcagatgtgcgaagacatgcccacatccagatcaagctgataccaccctct 660  
QY 688 cagggaagctgtatccgcgcacatgctctctcaaaaaaagctgacagctcaggaagt 747  
DB 661 cagggaagctgtatccgcgcacatgctctctctcaaaaaaagctgacagctcaggaagt 720  
QY 748 gtcgaagcgtgtcccaacacatagctgagccgttgatcaacaggaagcagatgtccct 807  
DB 721 gtcgaagcgtgtcccaacacatagctgagccgttgatcaacaggaagcagatgtccct 780  
QY 808 cctagtcatttgatctgagtagaaggaagacagcctatgcccagatgtatgaagatccatc 867  
DB 781 cctagtcatttgatctgagtagaaggaagacagcctatgcccagatgtatgaagatccatc 840  
QY 868 acaggaagaacagagctgtcgtgacatgagccacccaggtgtgacatgaaatcacg 927  
DB 841 acggaagaagcagagctgtcgtgacatgagccacccaggtgtgacatgaaatcacg 900  
QY 928 acagctctgtacaatttcatgtgtacacagcagctgtgttgaggaagatgaaccgcgtcca 987  
DB 901 acagctctgtacaatttcatgtgtacacagcagctgtgttgaggaagatgaaccgcgtcca 960  
QY 988 atttaacatgttactctctggaacacagatgaggaagctcctgagccagctctctt 1047  
DB 961 atttaacatgttactctctggaacacagatgaggaagctcctgagccagctctctt 1020  
QY 1048 gaggcccgatctgtgcttgcgcgaagaagacagagagcgagatgagatagatcaga 1107  
DB 1021 gaggcccgatctgtgcttgcgcgaagaagacagagagcgagatgagatagatcaga 1080  
QY 1108 aagcagcaggttctgagcagatcaaaagaacggtgagctgacgaagcgccgttcgtcag 1167  
DB 1081 aagcagcaggttctgagcagatcaaaagaacggtgagctgacgaagcgccgttcgtcag 1128  
QY 1168 aacacacatgtatccagatgacatccatcaagaagaacatcccaagatgagatgactg 1227  
DB 1129 aacacacatgtatccagatgacatccatcaagaagaacatcccaagatgagatgactg 1188  
QY 1228 ttatactacagatgagagcggtgagacatgaaatgagctgtgaaatgaaatgaaatgaa 1287  
DB 1189 ctgtacactacagatgagagcggtgagacatgaaatgagctgtgaaatgaaatgaaatgaa 1248  
QY 1288 ctggaacatcagcagatcctcctcagcacaacatgtgaacgctacaggaacagcag 1347  
DB 1249 ctggaacatcagcagatcctcctcagcacaacatgtgaacgctacaggaacagcag 1308  
QY 1348 cagcagacacacagcacttactcagagaacatctccttcagagccttcagagaatgagct 1407  
DB 1309 cagcagacacacagcacttactcagagaacatctccttcagagccttcagagaatgagct 1368  
QY 1408 gtcgaagcccgagagaagaatcccaaacatctgacgtctctctttagacatctccaaagcc 1467  
DB 1369 gtcgaagcccgagagaagaatcccaaacatctgacgtctctctttagacatctccaaagcc 1428  
QY 1468 ccaaacagatcagtgatcccatag 1491  
DB 1429 ccaaacagatcagtgatcccatag 1452

DB 541 ttccagcagtcagacacccagctcgcacccctgagcgttccacgtgaactgaagaagaa 600  
QY 628 ctctactgcaaatctgcaagacatgcccacatccagatcaagctgataccaccctct 687  
DB 601 cgttactgcagatgtgcgaagacatgcccacatccagatcaagctgataccaccctct 660  
QY 688 cagggaagctgtatccgcgcacatgctctctcaaaaaaagctgacagctcaggaagt 747  
DB 661 cagggaagctgtatccgcgcacatgctctctctcaaaaaaagctgacagctcaggaagt 720  
QY 748 gtcgaagcgtgtcccaacacatagctgagccgttgatcaacaggaagcagatgtccct 807  
DB 721 gtcgaagcgtgtcccaacacatagctgagccgttgatcaacaggaagcagatgtccct 780  
QY 808 cctagtcatttgatctgagtagaaggaagacagcctatgcccagatgtatgaagatccatc 867  
DB 781 cctagtcatttgatctgagtagaaggaagacagcctatgcccagatgtatgaagatccatc 840  
QY 868 acaggaagaacagagctgtcgtgacatgagccacccaggtgtgacatgaaatcacg 927  
DB 841 acggaagaagcagagctgtcgtgacatgagccacccaggtgtgacatgaaatcacg 900  
QY 928 acagctctgtacaatttcatgtgtacacagcagctgtgttgaggaagatgaaccgcgtcca 987  
DB 901 acagctctgtacaatttcatgtgtacacagcagctgtgttgaggaagatgaaccgcgtcca 960  
QY 988 atttaacatgttactctctggaacacagatgaggaagctcctgagccagctctctt 1047  
DB 961 atttaacatgttactctctggaacacagatgaggaagctcctgagccagctctctt 1020  
QY 1048 gaggcccgatctgtgcttgcgcgaagaagacagagagcgagatgagatagatcaga 1107  
DB 1021 gaggcccgatctgtgcttgcgcgaagaagacagagagcgagatgagatagatcaga 1080  
QY 1108 aagcagcaggttctgagcagatcaaaagaacggtgagctgacgaagcgccgttcgtcag 1167  
DB 1081 aagcagcaggttctgagcagatcaaaagaacggtgagctgacgaagcgccgttcgtcag 1128  
QY 1168 aacacacatgtatccagatgacatccatcaagaagaacatcccaagatgagatgactg 1227  
DB 1129 aacacacatgtatccagatgacatccatcaagaagaacatcccaagatgagatgactg 1188  
QY 1228 ttatactacagatgagagcggtgagacatgaaatgagctgtgaaatgaaatgaaatgaa 1287  
DB 1189 ctgtacactacagatgagagcggtgagacatgaaatgagctgtgaaatgaaatgaaatgaa 1248  
QY 1288 ctggaacatcagcagatcctcctcagcacaacatgtgaacgctacaggaacagcag 1347  
DB 1249 ctggaacatcagcagatcctcctcagcacaacatgtgaacgctacaggaacagcag 1308  
QY 1348 cagcagacacacagcacttactcagagaacatctccttcagagccttcagagaatgagct 1407  
DB 1309 cagcagacacacagcacttactcagagaacatctccttcagagccttcagagaatgagct 1368  
QY 1408 gtcgaagcccgagagaagaatcccaaacatctgacgtctctctttagacatctccaaagcc 1467  
DB 1369 gtcgaagcccgagagaagaatcccaaacatctgacgtctctctttagacatctccaaagcc 1428  
QY 1468 ccaaacagatcagtgatcccatag 1491  
DB 1429 ccaaacagatcagtgatcccatag 1452

RESULT 12  
AAX58577  
ID AAX58577 standard; cDNA; 2043 BP.  
XX AAX58577;  
AC AAX58577;  
XX 16-AUG-1999 (first entry)  
DT 16-AUG-1999 (first entry)  
XX Human cell regulatory protein p63, isoform deltaNp63 gamma, cDNA.  
XX

KW Cell regulatory protein; p63; hu-deltaNp63 gamma; human;  
 KW cancer; tumour suppressor; cell cycle control; apoptosis;  
 KW cell proliferation; cell differentiation; therapy; ss.  
 XX  
 OS Homo sapiens.  
 PN MO9919357-A2.  
 PD 22-APR-1999.  
 XX  
 PF 02-OCT-1998; 98WO-US21992.  
 XX  
 PR 29-MAY-1998; 98US-0087216.  
 PR 15-OCT-1997; 97US-0062076.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 PI McKeeon F, Yang A;  
 DR MPI: 1999-277595/23.  
 DR P-PSDB; MAY05958.  
 XX  
 PT New isolated p63 cell regulatory protein for, e.g. treatment of  
 PT tumours  
 PS  
 PS Claim 1; Fig 14; 161pp; English.  
 XX  
 CC The present invention concerns the discovery of a new family of  
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,  
 CC which demonstrate certain sequence identity to known tumour  
 CC suppressor proteins p53 and p73. It has been observed that the  
 CC intron-exon organisation is conserved between p73 and p53, and from  
 CC known exon and intron sizes for these 2 genes, it was possible to  
 CC identify new members of this gene family using a PCR-based strategy  
 CC of amplifying 2 exons in a conserved domain and their intervening  
 CC intron. The human p53 gene was localised to chromosomal position  
 CC 3q27-29. At least 6 different isoforms exist. Splice variants  
 CC differing at the C-terminus have been designated as alpha, beta and  
 CC gamma forms, while p63 members differing in the N-terminus are  
 CC designated as deltaN and TR forms, where the deltaN form lacks the  
 CC transactivation domain. The present sequence represents a cDNA  
 CC clone encoding human deltaNp63 gamma. p63 was detected in a variety  
 CC of human and mouse tissue. It demonstrates remarkably divergent  
 CC activities, such as the ability to transactivate p53 reporter genes  
 CC and induce apoptosis. Cessation or down-regulation of p63 expression  
 CC may play a critical role in the process of cervical squamous  
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63  
 CC act as dominant negatives towards transactivation by p53 and p63.  
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.  
 CC cachexia) and neuronal differentiation and related degenerative  
 CC disorders. p63 polypeptides (see MAY05953-64), polynucleotides (see  
 CC AA58572-83) and anti-p63 antibodies of the invention can be used to  
 CC identify compounds useful for treating disorders involving such  
 CC processes, in detection and diagnosis, and in the production of  
 CC transgenic animals.  
 CC  
 XX  
 SO Sequence 2043 BP; 536 A; 623 C; 471 G; 413 T; 0 other:

Query Match 41.0%; Score 1154.6; DB 20; Length 2043;  
 Best Local Similarity 91.5%; Pred. No. 0;  
 Matches 1234; Conservative 0; Mismatches 114; Indels 1; Gaps 1;

Db 121 tcgcagagaccacagacaagcgagttctcagccagaggtctccagacatactcggat 180  
 QY 208 ttctcggaaacacccatatagttcagttcagccacttgacttgacttggtgaatacca 267  
 Db 181 ttctcggaaacacccatatagttcagttcagccacttgacttgacttggtgaatacca 240  
 QY 268 tcagaagatggtgcagcaacaacaagattgagattagatgagctgatactcgatcgagac 327  
 Db 241 tcggaataatggtgcagcaacaacaagattgagattagatgagctgatactcgatcgagac 300  
 QY 328 tcggaacttgatgaccccaatgtgccaagatagacgaactcgtgggtccctgaacagatg 387  
 Db 301 tcagaacttgatgaccccaatgtgccaagatagacgaactcgtgggtccctgaacagatg 360  
 QY 388 gaccagcagattcagaagaagcgctcctcgtccaccagttccctataacaacagacgcgcag 447  
 Db 361 gaccagcagattcagaagaagcgctcctcgtccaccagttccctataacaacagacgcgcag 420  
 QY 448 aacagcgtcagcgccgcctcgcctcagcagacagccagctccacttcgattcgtctctct 507  
 Db 421 aatagcgtcagcgccgcctcgcctcagcagacagccagctccacttcgattcgtctctct 480  
 QY 508 ccataccgccgcctccctcccaacacccagctacccagcgcgcagattcgcagctgtctcc 567  
 Db 481 ccataccgccgcctccctcccaacacccagctacccagcgcgcagattcgcagctgtctcc 540  
 QY 568 ttccagcagtcgagacacgcgaagtgcgcacctcgtgacgtattccactgtaactgaagaaa 627  
 Db 541 ttccagcagtcgagacacgcgaagtgcgcacctcgtgacgtattccactgtaactgaagaaa 600  
 QY 628 ctctctcgaacttgcaagaagcagatgcgcctccatccagatgaagttatgagccccact 687  
 Db 601 ctgtactcgaacttgcaagaagcagatgcgcctccatccagatgaagttatgagccccact 660  
 QY 688 caggagagcgttatccgcgcacatgtcctgtctacaaaaagcgcgaacagtcacaggaagtg 747  
 Db 661 caggagagcgttatccgcgcacatgtcctgtctacaaaaagcgcgaacagtcacaggaagtg 720  
 QY 748 gtgaagcgtgtgccccaacacatgaagctgagcgtgaattcaagaaggagaaagattgcctc 807  
 Db 721 gtgaagcgtgtgccccaacacatgaagctgagcgtgaattcaagaaggagaaagattgcctc 780  
 QY 808 cctaagctattgattcgaatgaaggaggaacagccatgccagattgataaagatccatcc 867  
 Db 781 cctaagctattgattcgaatgaaggaggaacagccatgccagattgataaagatccatcc 840  
 QY 868 acaggaagacagagatgtgtgtgtaccttaagccacccacaggttggcactgaattcacg 927  
 Db 841 acaggaagacagagatgtgtgtgtaccttaagccacccacaggttggcactgaattcacg 900  
 QY 928 acagtcctgtataacttcaatgtgtatacagcagatgtgtgtgagggatgaacccgcgtcca 987  
 Db 901 acagtcctgtataacttcaatgtgtatacagcagatgtgtgtgagggatgaacccgcgtcca 960  
 QY 988 attttaatcatgttactcttgaaacccaagaattgggcaagctctctggccagacgtcgttt 1047  
 Db 961 attttaatcatgttactcttgaaacccaagaattgggcaagctctctggccagacgtcgttt 1020  
 QY 1048 gaggccggatctcgtcgtcgtcccaagaagaacgaaggcgtgataagatagatcacaga 1107  
 Db 1021 gaggccggatctcgtcgtcgtcgtcccaagaagaacgaaggcgtgataagatagatcacaga 1080  
 QY 1108 aagcagcaagattcgtgacagatcaaaagacggtgtagtgaagcgcgcgttctcgtccag 1167  
 Db 1081 aagcagcaagattcgtgacagatcaaaagacggtgtagtgaagcgcgcgttctcgtccag 1140  
 QY 1168 aacacacatgataccagatgacatccatcaagaagaacgaagatccccaagatgataacg 1227  
 Db 1141 aatacacacatgataccagatgacatccatcaagaagaacgaagatccccaagatgataacg 1200  
 QY 1228 ttatactacagtgaggggcgttgagacttaagaatgtctgtgaagatacaaaagatcc 1287  
 Db 1201 ctgtacctacagtgaggggcgttgagacttaagaatgtctgtgaagatacaaaagatcc 1260

Oy	1288	ctggaactcatgacgtagctacctctctcagacacacaattgaaacgtagcagacagcaaacag	1347
Db	1261	ctggagcctcatgacgtagctacctctctcagacacagcatcgaaacgtagcagcagcagcagcag	1320
Oy	1348	cagcagcacacgacactactctcagaaca	1376
Db	1321	cagcagcacacgacactactctcagaaca	1349
RESULT 13			
AA558576	AA558576		
ID	AA558576 standard; cDNA; 1182 BP.		
XX	AA558576;		
AC	16-AUG-1999 (first entry)		
DT			
XX			
DE	Human cell regulatory protein p63, isoform deltaNp63 beta, cDNA.		
XX			
KW	Cell regulatory protein; p63; hu-deltaNp63 beta; human;		
KW	cancer; tumour suppressor; cell cycle control; apoptosis;		
KW	cell proliferation; cell differentiation; therapy; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W09919357-A2.		
XX			
PD	22-APR-1999.		
XX			
PF	02-OCT-1998; 98WO-US21992.		
XX			
PR	29-MAY-1998; 98US-0082716.		
XX	15-OCT-1997; 97US-0062076.		
PA	(HARD ) HARVARD COLLEGE.		
XX			
PI	McKeon F, Yang A;		
XX			
DR	WPI: 1999-277595/23.		
XX			
DR	P-PSDB; AAY05957.		
XX			
PT	New isolated p63 cell regulatory protein for, e.g. treatment of		
PT	tumours		
XX			
XX	Claim 1; Fig 13; 161pp; English.		
XX			
CC	The present invention concerns the discovery of a new family of		
CC	cell regulatory proteins (CRPs) termed the p63 family of proteins,		
CC	which demonstrate certain sequence identity to known tumour		
CC	suppressor proteins p53 and p73. It has been observed that the		
CC	intron-exon organisation is conserved between p73 and p53, and from		
CC	known exon and intron sizes for these 2 genes, it was possible to		
CC	identify new members of this gene family using a PCR-based strategy		
CC	of amplifying 2 exons in a conserved domain and their intervening		
CC	intron. The human p53 gene was localised to chromosomal position		
CC	3q27-29. At least 6 different isoforms exist. Splice variants		
CC	differing at the C-terminus have been designated as alpha, beta and		
CC	gamma forms, while p63 members differing in the N-terminus are		
CC	designated as deltaN and TA forms, where the deltaN form lacks the		
CC	transactivation domain. The present sequence represents a cDNA		
CC	clone encoding human deltaNp63 beta. p63 was detected in a variety		
CC	of human and mouse tissue. It demonstrates remarkably divergent		
CC	activities, such as the ability to transactivate p53 reporter genes		
CC	and induce apoptosis. Cessation or down-regulation of p63 expression		
CC	may play a critical role in the process of cervical squamous		
CC	differentiation, both benign and neoplastic. DeltaN isoforms of p63		
CC	act as dominant negatives towards transactivation by p53 and p63.		
CC	p63 may also be implicated in haematopoiesis, muscle wasting (e.g.		
CC	cachexia) and neuronal differentiation and related degenerative		
CC	disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see		
CC	AA558572-83) and anti-p63 antibodies of the invention can be used to		
CC	identify compounds useful for treating disorders involving such		

CC processes, in detection and diagnosis, and in the production of  
CC transgenic animals.  
XX  
SQ Sequence 1182 BP; 330 A; 342 C; 276 G; 234 T; 0 other;

Query Match	40.6%	Score 1143.6	DB 20	Length 1182
Best Local Similarity	98.4%	Pred. No. 0		
Matches 1155; Conservative	0	Mismatches 19	Indels 0	Gaps 0

OY	318	caagagagaaacccgagaccctgaaatgaaacccaatgtgcccagatcaacgaaactgggctctc	3777
Db	9	ccctggaaaaacaatgcccagagactcaatttgaatgagcccaagatcacgaaactggtgctctc	68
OY	378	gaacagcgaatggaaacagcagatcttcgaagaaggtctctctgtccaaagtccctataacaga	4373
Db	69	gaacagcgaatggaaacagcagatcttcgaagaaggtctctctgtccaaagtccctataacaga	1287
OY	438	ccaaagcgaagaacagcgtlcaacggtccctctgcccataagcagaagccagctccaaacttga	497
Db	129	ccaaagcgaagaacagcgtlcaacggtccctctgcccataagcagaagccagctccaaacttga	188
OY	498	tgctctctcttcataccacccgcatccctccaaacccgactaaccagcccgcaagttt	5577
Db	189	tgctctctcttcataccacccgcatccctccaaacccgactaaccagcccgcaagttt	248
OY	558	cgaagtgctccttcacagcagatcgagacaacgccaagtctgcacactggaagcgtatccactga	6177
Db	249	cgaagtgctccttcacagcagatcgagacaacgccaagtctgcacactggaagcgtatccactga	308
OY	618	acgtgaagaagaacttaactctgcacaatltgcagaagacaatgcccataccagaatcaaggtga	6777
Db	309	acgtgaagaagaacttaactctgcacaatltgcagaagacaatgcccataccagaatgtgaac	368
OY	678	cccaacccctccataaggagactgttatccgcgcgaatgcgtcttcaaaaaagctgaacagct	737
Db	369	cccaacccctccataaggagactgttatccgcgcgaatgcgtcttcaaaaaagctgaacagct	428
OY	738	caacgagatgtgtgaagagcgtgtgcccccaacaaatgaagcttgaagcgtgaattcaacgaagga	797
Db	429	caacgagatgtgtgaagagcgtgtgcccccaacaaatgaagcttgaagcgtgaattcaacgaagga	488
OY	798	gattgccccctctcagatcatcttgaatctgcagatagaaggggaacagccatgcccagatgtaga	857
Db	489	gattgccccctctcagatcatcttgaatctgcagatagaaggggaacagccatgcccagatgtaga	548
OY	858	agatccccatcaacaggaagacaagatgtgtgcgttaacctatgaagccaaacccaggttgacac	917
Db	549	agatccccatcaacaggaagacaagatgtgtgcgttaacctatgaagccaaacccaggttgacac	608
OY	918	tgaattcaagacagctctgtfacaaatttcagatgtgttaacagaagtgtgttggagagatga	977
Db	609	tgaattcaagacagctctgtfacaaatttcagatgtgttaacagaagatgtgttggagagatga	668
OY	978	ccgcgcgtccaaatttlaatacatgttlaactctgcgaagaacagaagatggtgccaagctctggccg	103
Db	669	ccgcgcgtccaaatttlaatacatgttlaactctgcgaagaacagaagatggtgccaagctctggccg	728
OY	1038	acgcgtcttggagggcccggatctgtgctgtgccaggaagagacaaggaagcggatgtaga	1097
Db	729	acgcgtcttggagggcccggatctgtgctgtgccaggaagagacaaggaagcggatgtaga	788
OY	1098	tgaacataagaagaacagcaaaatttcggaaacggtataaagaacggtgtgattgtgtacgaagccgc	1157
Db	789	tgaacataagaagaacagcaaaatttcggaaacggtataaagaacggtgtgattgtgtacgaagccgc	848
OY	1158	gtttcgttcagaagaacacatgtgtatccagaatgaacatccatcaagaagaacggaagatccccaga	1217
Db	849	gtttcgttcagaagaacacatgtgtatccagaatgaacatccatcaagaagaacggaagatccccaga	908
OY	1218	tgaatgaactgtatactatctcaagtgaaagggccgtgagactatgaatgtcgttgtagaat	1277
Db	909	tgaatgaactgtatactatctcaagtgaaagggccgtgagactatgaatgtcgttgtagaat	968



Qy	1278	caagaagatcccttggaactcatgcatgtaaccttcctcctaagcagcacacaattgaaagctaacagca	1337
Db	969	caaaagatccctctggaactcatgcatgtaaccttcctcctaagcagcacacaattgaaagctaacagca	1028b
Qy	1338	acagcaacagcagaacagacacgaacacttactttagaagaacatccctcttaagctgctttag	1397
Db	1029	acagcaacagcagaacagacacgaacacttactttagaagaacatccctctttagcctgctttag	1088b
Qy	1398	gaatgagctctgtgagagcccccggagagagaacatccaaacatcttgacgctctctttagaca	1457
Db	1089	gaatgagctctgtgagagcccccggagagagaacatccaaacatcttgacgctctctttagaca	1148b
Qy	1458	ttccaagcccccaaacgcgatcatgtgtacccatag	1491
Db	1149	ttccaagcccccaaacgcgatcatgtgtacccatag	1182

RESULT	14
AA227674	
ID	AA227674 standard; DNA; 2082 BP.

DT 20-DEC-1999 (first entry)

Human p40 coding sequence.

Human; p40; p53 homologue; oncogene; diagnosis; proliferative disease; anticancer therapeutic identification; cancer; immunogen; neoplasia; immunoassay reagent; tumour; dysplasia; hyperplasia; therapy; ss.

aa  
OS Homo sapiens.

AA  
PN W09950287-A2.

XX  
PD 07-OCT-1999.

XX 26-MAR-1999: 99WO-US06657.  
PF

XX 27-MAR-1998: 98MS-0079736  
PR

XX /TV.TV \ INTV .JOHNS HOPKINS  
DA

XX  
DT  
Eriqle B  
Tos T  
B+ C+ I + Ck! E  
C Y J  
S S  
L L  
J

XX  
XX  
1000-80133400

DR P-PSDB; AAY43135.

PT Isolated oncoproteins used to classify and diagnose tumours, and in

XX XX

This sequence encodes the human p40 protein of the invention. p40 (the shortest variant of a new human p53 homologue) is oncogenic and detection of its overexpression (at protein or nucleic acid levels) is used to diagnose and classify cancers or other proliferative diseases. It can also be used to identify agents, potential anticancer therapeutics, that modulates its binding to p53. p40 (or its fragments or fusion proteins) are used as immunogens to raise (or to purify) antibodies. Antibodies are used as immunoassays reagents for detecting overexpression of p40, also therapeutically against tumours. Fragments of the nucleic acid that encode p40 are used for recombinant expression; as probes to quantify p40 gene expression or to identify related sequences; as probes to quantify p40 antisense fragments are useful for inhibiting expression of p40, for treatment of neoplasia, dysplasia and hyperplasia.

Sequence 2082 BP; 605 A; 493 C; 473 G; 511 T; 0 other;

**Query Match**

Best Local Similarity 95.78; Pred. No. 2e-277;

Matches 1060; Conservative 0; Mismatches 48; Indels 0; Gaps. 0;

OY	269	cagaagatggtgogacaacaagaatggagattgacatgagacgtgatccgatgcagagagct	328
Db	395	cagagaagaagagacgcgcgatctgataacttcttaagctaacatgctgtgtacccaggaaaca	454
OY	329	cgagaccgtgagagaccoccatgctggccacaagatatacagaaactctgggctccctgtaacatactg	388
Db	455	atgcgccagactcgaatttagtggagccaaatgatacagaaactctgggctctctgaaacagcatgg	514
OY	389	accagagatctagaacagctcctcgttccacagatccctataacaaagacacgcgcgaca	448
Db	515	accagagatctacaagagctcctcgttccacagatccctataacaaagacacgcgcgaca	574
OY	449	acagcgttcaacggccctctgcctcttaagcagaagccagagctccacactctgatgtctcttc	508
Db	575	acagcgttcaacggccctctgcctcttaagcagaagccagagctccacactctgatgtctcttc	634
OY	509	catcacccgcacatccctctccacacagactataccacaagcccgacagttctgcagctgtcct	568
Db	635	catcacccgcacatccctctccacacagactataccacaagcccgacagttctgcagctgtcct	694
OY	559	tccagcagctcgagagacccgcgaagtctggccacctcgagcgtatctccactgacatgaaagaac	628
Db	695	tccagcagctcgagagacccgcgaagtctggccacctcgagcgtatctccactgacatgaaagaac	754
OY	629	tctactgcacaattgacaaagacatgccccatccagatcgaagtgtatgaaagccacactcttc	688
Db	755	tctactgcacaattgacaaagacatgccccatccagatcgaagtgtatgaaagccacactcttc	814
OY	689	agggagctgltatccgcgcgcacgtcgtctataaaaaagctgaagcactacagagatgtg	748
Db	815	agggagctgltatccgcgcgcacgtcgtctataaaaaagctgaagcactacagagatgtg	874
OY	749	tgaagcggtgtgcccaacacagagctgaagccgtgtaattccaagcagaggaacagatctgccttc	808
Db	875	tgaagcggtgtgcccaacacagagctgaagccgtgtaattccaagcagaggaacagatctgccttc	934
OY	809	ctaactcatcttgatctcgagtagagagggaacagccatgcccagatgtlaagagaatcccatca	868
Db	935	ctaactcatcttgatctcgagtagagagggaacagccatgcccagatgtlaagagaatcccatca	994
OY	869	caggaagaacagagatgtcgtgtgatacctatagagccaccccaagtttgccactgataatcaaga	928
Db	995	caggaagaacagagatgtcgtgtgatacctatagagccaccccaagtttgccactgataatcaaga	1054
OY	929	cagctctgtacaactcttaactgtgtataacacagcagttgtgttgagagatgtaaacccgcgtcca	988
Db	1055	cagctctgtacaactcttaactgtgtataacacagcagttgtgttgagagatgtaaacccgcgtcca	1114
OY	989	ctttaatcatctgtactctctggaacaacagagatgaggcaagtcctgggcgacgcgtcttg	1048
Db	1115	ctttaatcatctgtactctctggaacaacagagatgaggcaagtcctgggcgacgcgtcttg	1174
OY	1049	agggccggatctgtgctctgtgcccggaagagaacagagccgagatgaagaaatagatacaaga	1108
Db	1175	agggccggatctgtgctctgtgcccggaagagaacagagccgagatgaagaaatagatacaaga	1233
OY	1109	agcagcaagcttcctggaacagatataaagaaacggtgtatgtatcgaagcgcgccgttctgtcca	1166
Db	1235	agcagcaagcttcctggaacagatataaagaaacggtgtatgtatcgaagcgcgccgttctgtcca	1294
OY	1159	acacacatggtatcccaatgtaacatccatacaagaacagaagatcccccagatgtgtgaactgt	1222
Db	1295	acacacatggtatcccaatgtaacatccatacaagaacagaagatcccccagatgtgtgaactgt	1354
OY	1229	tatacttaccagtgaaagggcgtgtagaactatgaaatgctgtgttgaagatccaagagctccc	1288
Db	1355	tatacttaccagtgaaagggcgtgtagaactatgaaatgctgtgttgaagatccaagagctccc	1414
OY	1289	tggaaactatgtagtacctctctcttaagacaacatgtgaaacgtatacaggaacacagacagc	1348
Db	1415	tggaaactatgtagtacctctctcttaagacaacatgtgaaacgtatacaggaacacagacagc	1474

OY 1349 agcagaccagactactcagaaca 1376  
|||||  
Db 1475 agcagaccagactactcagaaca 1502

## RESULT 15

AAAC6030  
ID AAC6030 standard; cDNA; 2082 BP.

AAAC6030;

21-FEB-2001 (first entry)

Human lung cancer-associated cDNA p63 isoform 4.

Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
vaccine; detection; ss.

OS Homo sapiens.

WO200061612-A2.

19-OCT-2000.

03-APR-2000; 2000MO-US08896.

02-APR-1999; 99US-0285479.

17-DEC-1999; 99US-0466396.

30-DEC-1999; 99US-0476496.

10-JAN-2000; 2000US-0480884.

22-FEB-2000; 2000US-0510376.

(CORI-) CORIXA CORP.

Wang T, Fan L;

WPI: 2000-628399/60.  
P-PSDB; AAB11360.

Isolated polypeptide comprising an immunogenic portion of a lung tumor  
protein is used for detecting and monitoring progression of lung cancer  
in a patient -

Claim 25a; Page 239-240; 261pp; English.

This invention describes a novel isolated polypeptide (1) which  
comprising an immunogenic portion of a lung tumor protein or variant (P2)  
which have cytostatic activity. The polypeptides and polynucleotides are  
used in compositions and vaccines to inhibit the development of cancer,  
especially lung cancer, in a patient. Methods described in the invention  
can be used to monitor the progression of a cancer by carrying out the  
detection at subsequent time points and comparing the results from the  
different time points. CD4+ and/or CD8+ T-Cells isolated from a patient  
are treated with P2, polynucleotides encoding P2 or antigen presenting  
cells expressing P2 and then administered to the patient to inhibit  
development of cancer.

Sequence 2082 BP: 605 A; 493 C; 473 G; 511 T; 0 other;

Query Match 36.6%; Score 1031.2; DB 21; Length 2082;  
Best Local Similarity 95.7%; Pred. No. 2e-277;

Matches 1060; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

OY 269 cagaagatggtgcgaacaagaatgagattagatgactgtatccgcatgagagact 328  
|||||  
Db 335 cagaagaagagacagcatgtatcattacagctaacatgtgttactgtgaaca 454

OY 329 cgaactgagtgaccccatgtgcccacagatcacgaacactggggctccctgaacagctg 388  
|||||  
Db 455 atgcccgactcaatttagtgaccacagatcacgaacacttgggtctctgaacagctg 514

OY 389 accagagattcagaacggctctctgcccacagttccctataacacagacagcgagca 448  
Db 515 accagagattcagaacggctctctgcccacagttccctataacacagacagcgagca 574  
OY 449 acaggtcagcagcgcctctgcccacagtcagcagcagcagcagcagcagcagcagc 508  
Db 575 acaggtcagcagcgcctctgcccacagtcagcagcagcagcagcagcagcagcagc 634  
OY 509 catcacccgcatccctctccacacagcagcagcagcagcagcagcagcagcagcagcagc 568  
Db 635 catcacccgcatccctctccacacagcagcagcagcagcagcagcagcagcagcagcagc 694  
OY 569 tccagcagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 628  
Db 695 tccagcagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 754  
OY 629 tctactgccaattgccaagacatgcccacatccagatcaaggtatgacccactctc 688  
Db 755 tctactgccaattgccaagacatgcccacatccagatcaaggtatgacccactctc 814  
OY 689 aggaagctgtatccgcgcacatgctgtctacaaaagagctgagcagcagcagcagcagc 748  
Db 815 aggaagctgtatccgcgcacatgctgtctacaaaagagctgagcagcagcagcagcagc 874  
OY 749 tgaagcgtgcccccaacatgagctgagcgtgaattcaacgagagacagatgcccctc 808  
Db 875 tgaagcgtgcccccaacatgagctgagcgtgaattcaacgagagacagatgcccctc 934  
OY 809 ctatgacttgatcgaatagagggagagcagcagcagcagcagcagcagcagcagcagcagc 868  
Db 935 ctatgacttgatcgaatagagggagagcagcagcagcagcagcagcagcagcagcagcagc 994  
OY 869 cagaagaacagatgtgtgtgtacattatgagccacacagcagcagcagcagcagcagcagc 928  
Db 995 cagaagaacagatgt 1054  
OY 929 cagcttgtaaatgttatgt 988  
Db 1055 cagcttgtaaatgttatgt 1114  
OY 989 tttaaatctgttactctgtgaacacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1048  
Db 1115 tttaaatctgttactctgtgaacacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1174  
OY 1049 aggcgcgagctgt 1108  
Db 1175 aggcgcgagctgt 1234  
OY 1109 agcagcagcttgcgacagatgacaagaacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1168  
Db 1235 agcagcagcttgcgacagatgacaagaacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1294  
OY 1169 acacacatgttaccagatgacatccatcaagaacagcagcagcagcagcagcagcagcagc 1228  
Db 1295 acacacatgttaccagatgacatccatcaagaacagcagcagcagcagcagcagcagcagc 1354  
OY 1229 tatacttaccagtgagggcggtgagactatgaagtgtgtgtgtgtgtgtgtgtgtgtgtgt 1288  
Db 1355 tatacttaccagtgagggcggtgagactatgaagtgtgtgtgtgtgtgtgtgtgtgtgtgt 1414  
OY 1289 tggaaactatgacagctctctcagcacacaaatgaaacgacagcagcagcagcagcagc 1348  
Db 1415 tggaaactatgacagctctctcagcacacaaatgaaacgacagcagcagcagcagcagcagc 1474  
OY 1349 agcagacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1376  
Db 1475 agcagacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1502

Search completed: August 8, 2001, 00:20:08  
Job time: 8139 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2001, 21:24:54 ; Search time 108.78 Seconds  
(Without alignments)  
4900.718 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816  
Sequence: 1 tcgtgatatacaagaacagt.....gcatttggttaaagaana 2816

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued\_Patents\_MA:\*
- 2: /cgml\_7/ptodata/1/ina/5A\_COMB.seq:\*
- 3: /cgml\_7/ptodata/1/ina/5B\_COMB.seq:\*
- 4: /cgml\_7/ptodata/1/ina/6A\_COMB.seq:\*
- 5: /cgml\_7/ptodata/1/ina/6B\_COMB.seq:\*
- 6: /cgml\_7/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244.2	8.7	1215	1	US-08-347-792-20 Sequence 20, Appl
2	244.2	8.7	1215	1	US-08-431-357-20 Sequence 20, Appl
3	244.2	8.7	1215	4	US-08-392-542-26 Sequence 26, Appl
4	244.2	8.7	1215	4	US-08-894-337-26 Sequence 26, Appl
5	244.2	8.7	1215	5	PCT-US95-15353-20 Sequence 20, Appl
6	242.6	8.6	1181	2	US-08-486-663A-18 Sequence 18, Appl
7	242.6	8.6	1181	2	US-08-247-904B-11 Sequence 11, Appl
8	242.6	8.6	1181	3	US-08-767-942A-22 Sequence 22, Appl
9	242.6	8.6	1182	2	US-08-184-009-215 Sequence 215, App
10	242.6	8.6	1182	2	US-08-484-956-92 Sequence 92, Appl
11	242.6	8.6	1182	2	US-08-484-956-94 Sequence 94, Appl
12	242.6	8.6	1182	2	US-08-757-653-92 Sequence 92, Appl
13	242.6	8.6	1182	2	US-08-757-653-94 Sequence 94, Appl
14	242.6	8.6	1182	2	US-08-458-356-215 Sequence 215, App
15	242.6	8.6	1182	4	US-08-796-101-46 Sequence 46, Appl
16	242.6	8.6	1303	1	US-08-047-041A-13 Sequence 13, Appl
17	242.6	8.6	1307	1	US-08-047-041A-12 Sequence 12, Appl
18	242.6	8.6	1317	1	US-07-912-011-1 Sequence 1, Appl
19	242.6	8.6	1317	1	US-08-347-792-1 Sequence 1, Appl
20	242.6	8.6	1317	1	US-08-431-357-1 Sequence 1, Appl
21	242.6	8.6	1317	2	US-08-697-221-1 Sequence 1, Appl
22	242.6	8.6	1317	4	US-08-392-542-1 Sequence 1, Appl
23	242.6	8.6	1317	4	US-08-894-337-1 Sequence 1, Appl
24	242.6	8.6	1317	5	PCT-US95-15353-1 Sequence 1, Appl
25	242.6	8.6	1483	4	US-08-796-101-44 Sequence 44, Appl
26	242.6	8.6	1484	2	US-08-184-009-103 Sequence 103, App
27	242.6	8.6	1484	2	US-08-458-356-103 Sequence 103, App

28	242.6	8.6	1511	4	US-08-796-101-168 Sequence 168, App
29	242.6	8.6	1512	2	US-08-184-009-99 Sequence 99, Appl
30	242.6	8.6	1512	2	US-08-458-356-99 Sequence 99, Appl
31	241	8.6	1182	2	US-08-484-956-93 Sequence 93, Appl
32	241	8.6	1182	2	US-08-757-653-93 Sequence 93, Appl
33	238.6	8.5	1355	2	US-08-636-376-1 Sequence 1, Appl
34	234.6	8.3	633	3	US-08-886-280-6 Sequence 6, Appl
35	234.6	8.3	633	3	US-08-870-370-10 Sequence 10, Appl
36	234.2	8.3	1173	2	US-08-184-009-214 Sequence 214, App
37	234.2	8.3	1173	2	US-08-458-356-214 Sequence 214, App
38	234.2	8.3	1173	4	US-08-796-101-45 Sequence 45, Appl
39	228.4	8.1	740	4	US-09-112-437-10 Sequence 10, Appl
40	220.8	7.8	601	2	US-08-484-956-107 Sequence 107, App
41	220.8	7.8	601	2	US-08-484-956-108 Sequence 108, App
42	220.8	7.8	601	2	US-08-757-653-107 Sequence 107, App
43	220.8	7.8	601	2	US-08-757-653-108 Sequence 108, App
44	219.2	7.8	601	2	US-08-484-956-97 Sequence 97, Appl
45	219.2	7.8	601	2	US-08-484-956-98 Sequence 98, Appl

ALIGNMENTS

RESULT 1  
US-08-347-792-20  
; Sequence 20, Application US/08347792  
; Patent No. 5573925  
; GENERAL INFORMATION:  
; APPLICANT: Halazometis, Thanos D.  
; TITLE OF INVENTION: p53 Proteins With Altered  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Howson and Howson  
; STREET: Spring House Corporate Cntr., PO Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,792  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9206  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1215 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-347-792-20

Query Match 8.7%; Score 244.2; DB 1; Length 1215;  
Best Local Similarity 58.3%; Pred.No. 6.4e-59;  
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 506 ctcacatccgcgcacccctccacacacgcgacgagccgcgacggttcgcgcggt 565  
DB 302 CCCTGTCATCTTCTGTCCTCCCTCCAGAAAACCTACAGGCGAGTACGCTTCCGCTGCG 361

```

QY 566 ccttcacagtcgagacacgcgaagtcggccaccctgacacgtatccactgaatgaaga 625
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 GCTTCTTGCAATCTGGAGACAGCCAACTCTGTACATTGCACTGCTCCCTGCCCTCAACA 421
QY 626 aactctactgccaatttgcgaagacatgcccacatccacatcaaggttgaatgccaccctc 685
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 ACATGTTTGGCCAACTGGCGAAGACCTGCCCTGTGACGCTGTGGGTTGATTCACACCCC 481
QY 686 ctcaaggaagctgtatccggccatgacgtcgttctacaataaactgaagcagtcgaagag 745
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 CCGCCGGGACCCGCGCTCCGCGCATGGCCATCTACAGCATACAGCATACGATGAGGAGG 541
QY 746 tgggtgaagcgtgtgcccacacacacacacacacacacacacacacacacacacacac 805
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 TTGTGAGGCGCTGCCCGCCCATGAGCGCGCTGCTCAGATAGCATG-----GTCTGGCCC 595
QY 806 ctccctagtcattgtatgtgagtagagggaggaacagccatgcccagatgtagaagatccca 865
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 596 CTCCCTCAGCATCTTATCCGATGGAAGAAATTTGCTGTGAGTATTTGATGACAGAA 655
QY 866 tcacaggaagacagagtgctgtgtacatctatgaagccacccaggttgcacatgaatca 925
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 656 ACACCTTTTGAATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 715
QY 926 cgacagctctgtacacatttcatatgttgaacagacagctgtgtgtgagagatgaacccgctc 985
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 716 CCACCATCTACATCAACATCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 775
QY 986 caatttatacttctgttactctgtgaacacacagatgaggaagtcctgtggcgcagcgtcgt 1045
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 776 CCATCTCTACCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 835
QY 1046 ttgagcccgagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1105
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 836 TTGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
QY 1106 gaaagcagcaagtttcgacagacacacacacacacacacacacacacacacacacac 1165
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 896 GCAAGAAAGGGAGGAGCTCAACGAGCTCCCGCCAGGGAGCACTAAGGAGCAGTGCCTCA 955
QY 1166 agaagacacatgtatcagatagacatccatcaagaacagaaatccacagatgtgtgaac 1225
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 956 ACAACAC-----CAGCTCTCTCCCGCCAGCCAAAGAAAGAAACCTGATGAGAGAT 1006
QY 1226 tgttacttaccagtgagggcgctgagacatctgaatgtgtgtgtgtgtgtgtgtgtgt 1285
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1007 ATTTCACCTTCAGATGCGGGGCGTGAAGCGCTTGAATGTTCCGAGAGCTGATGAGG 1066
QY 1286 cccttgaaactatgtacatccttctcagca 1316
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1067 CCTTGGAACTCAAGATGCGCCAGGCTGGGAA 1097

```

```

RESULT 2
US-08-431-357-20
: Sequence 20, Application US/08431357
: Patent No. 5721340
: GENERAL INFORMATION:
: APPLICANT: Halazometis, Thanos D.
: TITLE OF INVENTION: p53 Proteins With Altered
: TITLE OF INVENTION: Tetramerization Domains
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Howson and Howson
: STREET: Spring House Corporate Cntr., PO Box 457
: CITY: Spring House
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19477
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/431,357
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/347,792
: FILING DATE: 28-NOV-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Bak, Mary E.
: REGISTRATION NUMBER: 31,215
: REFERENCE/DOCKET NUMBER: WST58USA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-540-9206
: TELEFAX: 215-540-5818
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1215 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-431-357-20

```

```

Query Match 8.7% Score 244.2; DB 1; Length 1215;
Best Local Similarity 58.3%; Pred. No. 6,46-59;
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

```

```

QY 506 ctccatcacccgcacatccctccacacacacacacacacacacacacacacacacacacac 565
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 CCGTGTCAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 361
QY 566 ccttcacagtcgagacacgcgaagtcggccaccctgacacgtatccactgaatgaaga 625
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 GCTTCTTGCAATCTGGAGACAGCCAACTCTGTACATTGCACTGCTCCCTGCCCTCAACA 421
QY 626 aactctactgccaatttgcgaagacatgcccacatccacatcaaggttgaatgccaccctc 685
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 ACATGTTTGGCCAACTGGCGAAGACCTGCCCTGTGACGCTGTGGGTTGATTCACACCCC 481
QY 686 ctcaaggaagctgtatccggccatgacgtcgttctacaataaactgaagcagtcgaagag 745
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 CCGCCGGGACCCGCGCTCCGCGCATGGCCATCTACAGCATACAGCATACGATGAGGAGG 541
QY 746 tgggtgaagcgtgtgcccacacacacacacacacacacacacacacacacacacacac 805
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 TTGTGAGGCGCTGCCCGCCCATGAGCGCGCTGCTCAGATAGCATG-----GTCTGGCCC 595
QY 806 ctccctagtcattgtatgtgagtagagggaggaacagccatgcccagatgtagaagatccca 865
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 596 CTCCCTCAGCATCTTATCCGATGGAAGAAATTTGCTGTGAGTATTTGATGACAGAA 655
QY 656 tcacaggaagacagagtgctgtgttaccttatagaacacccacaggttgcacatgaatca 925
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 656 ACACCTTTTGAATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 715
QY 926 cgacagctctgtacacatttcatatgttgaacacacacacacacacacacacacacacac 985
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 716 CCACCATCTACATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 775
QY 986 caatttatacttctgttactctgtgaacacacacacacacacacacacacacacacacacac 1045
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 776 CCATCTCTACATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 835
QY 1046 ttgagcccgagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1105
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 836 TTGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
QY 1106 gaaagcagcaagtttcgacagacacacacacacacacacacacacacacacacacac 1165
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 896 GCAAGAAAGGGAGGAGCTCAACGAGCTCCCGCCAGGGAGCACTAAGGAGCAGTGCCTCA 955

```

QY 1166 agcacacactgtgtatccagatgacatccatcaagaagaagatccccagatgtgtac 1225  
 || |||||  
 Db 956 ACAACAC-----CAGCTCTCTTCCACAGCCAAAGAAGAAACACTGTGTGAGAT 1006  
 QY 1226 ttttatcttaccagtgagggcgctgagactatgaatgtgttgaagtcaagaagt 1285  
 |||||  
 Db 1007 ATTTCACCCCTTCAGATTCGGGGGCGAGACGCTTCACAAATGTTCCGAGAGCTGAATGAGG 1066  
 QY 1286 ccttgagactcatgcagtagtaacctcttcacga 1316  
 |||||  
 Db 1067 CTTGGAACTCAAGATGCCCAAGCTGGGAA 1097

### RESULT 3

```

US-08-392-542-26
Sequence 26, Application US/08392542
Patent No. 6169073
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
TITLE OF INVENTION: Peptides nad Peptidomimetics with
TITLE OF INVENTION: Structural Similarity to Human p53 That Activate p53
TITLE OF INVENTION: Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,542
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-392-542-26

```

Query Match	8.78;	Score 244.2;	DB 4;	Length 1215;
Best Local Similarity	58.38;	Pred. No. 6.4e-59;		
Matches 473; Conservative	0;	Mismatches 333;	Indels 15;	Gaps 2

QY	506	ctccatataccgcgcattccctcccaacacgcgactatcccgagcccgcaagtttgaagttg	5655
Db	302	CCCTGTATCTTCTGTCCCTTCCAGAAAACCTACACGGGACAGCTAAGTTCCTGTGG	3611
QY	566	ctcttcagcagtcgacgaccgcgaagtcgagccacttgagctatltccactgaaactgaaga	6253
Db	362	GCTTCTTGCAATTCTGGGACACCCAAAGTCTGTGAATTTCACAGTACTGCCCTTCACAA	4211
QY	626	aactctactgcgaattgcaagaagacatgccccatccagatcaagtgatgacccaccctc	6855

Db	422	AGATGTTTGGCAACATGGCAAAAGACTGCCCTGTGAGCTGTGGGTATGATTCACACCCC	481
Oy	686	ctcaggaagcgtgtatccgcgcacatgcgcgtgtctacaanaagctgagcagctcagsgag	745
Db	482	CGCCGGCACCACCGCGTCCGGCCATGGCCATACAGCAAGTCACAGCAACATGACGAGAG	541
Oy	746	tgtgtgaagcggtgcccacacatgaactgaagcgtgaatcttaagaaggaaacagctggcc	805
Db	542	TTGTGAGGCGGTGGCCCCACCATGAGCGCTGCTCAATAGCAATG-----GTCGTGGCC	595
Oy	806	ctccctagctatcttgatctcgatgaaggaggaaacacatgtcccagatgtlagaagaatccca	865
Db	596	CTCCCTCAGCATCTTATTCGAGTGGAGGAATAATTGCGTGGAGATATTGGATGACAGA	655
Oy	866	tcaacaggaagaacagagtgctgtctgtatcctatgaagccacccaggttggcaactgaatcca	925
Db	656	ACACTTTTTCGCATAGTGTGTGTATCCCTCATGAGCGCGCTGAGGTGGCTCTGACTCTTA	715
Oy	926	cgacagctctgtacaattctatgtlgtacaacagcagctgtgtttgaaggatgaacccgcgtc	985
Db	716	CCACATCTCACTACACTTACATATGTGTAACAGTTCCCTGCATGGGGCGGACATGAACCGGAGGC	775
Oy	986	caatttaatcatctgttaactctctgtgaaacacagatgaggcaagctcctgggcgagcgtct	1045
Db	776	CCATCTCCACCATCATATCACTGGAAGACTCCAGTGTGATCTACTGGGACCGCAACACT	835
Oy	1046	ttgtagcccgagatctgtgtctctggccaggaagacaggaaggcggatgaagaatgacatcca	1105
Db	836	TTTGAGGTGCGTGTGTTGTGCTGTGCTGTGGAGAACCGCGCCACAGAGAGAGAAATCTCC	895
Oy	1106	gaaagcagcaagcttctggacagtacaagaagaacggtlgtatgtacgaagcgcccgttctgc	1165
Db	896	GCAAGAAAGGGGAGACCTCACACAGAGCTCCCCCAGGAGGACCTAAAGCAGACATGCCCA	955
Oy	1166	agaacacacatgtatctccagaatgaatccaagaagaagaatccccagatgtatgac	1225
Db	956	ACAACAC-----CAGCTCCTCTCCCCAGGCCAAAGAAAGAAACCACTGCTGTGGAGAT	1006
Oy	1226	tgtataacttaccagltgaggcgctgtgagactatataaigtctgttgaagatcaaaaggt	1285
Db	1007	ATTTCACCCCTTCAAGATCCGGGGGCGTAGGAGCGCTTCGAATGTTCCGAGAGCTGATGAGG	1066
Oy	1286	ccctgtgaactcatgctgaactctctcagca	1316
Db	1067	CGTTGGAACCTAAAGATGCCCAAGCTGTGGAA	1097

## RESULT 4

US-08-894-327-26  
Sequence 26. Application US/08894327  
Patent No. 6245886  
GENERAL INFORMATION:  
APPLICANT: Halazonetis, Thanos  
TITLE OF INVENTION: Peptides and peptidomimetics with  
TITLE OF INVENTION: structural similarity to human p53 that activate p53  
TITLE OF INVENTION: function  
FILE REFERENCE: 2973.19998  
CURRENT APPLICATION NUMBER: US/08/894,327  
CURRENT FILING DATE: 1997-12-04  
EARLIER APPLICATION NUMBER: pctus96/01555  
EARLIER FILING DATE: 1996-02-16  
EARLIER APPLICATION NUMBER: 08/392,542  
EARLIER FILING DATE: 1995-02-16  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 1215  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-08-894-327-26

```

Query Match      8.7%; Score 244.2; DB 4; Length 1215;
Best Local Similarity 58.3%; Pred. No. 6.4e-59;
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 506 ctccatccacgcgcacatccctcccaacaacgcagaccagccgcagcagtttcagcgt 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 302 cccctgtatctctgtccctcccaaaaacccacagcgagcagcttcgtcgtg 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 566 ccttcagcagtcgagcagccagtcgcccagtcgagctatccactgaactgaaga 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 362 gctcttgcatcttgagcagccaactctgtgacttgcaactccctccgcctcaaca 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 626 aactctactgccaacttgcaagacatgcccattccagatcaagtgatgacccacc 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 422 agatgttttcgcaactgagcaagacctgtgcacctgtgagtggttgattccacccc 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 686 ctgagggagctgtatccgcgcacatgctcgtctacaaaaagctgagcagtgagg 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 482 cgcgcgagccgcgcgtccgcgcagtcagcatctacagcagtcacagcacatgacgag 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 746 tggtagagcggtgcccacacatgagctgagccgtgtaattcaacgagggacagattgcc 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 542 ttgtgagggcgctgcccacacatgagcgtctgcagatagcagtg------gtcggccc 595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 806 ctctcagtcatttgatcgagtagagggagcaagccatgcccaglatgtagaagatccca 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 596 ctctcagcatcttaccgagtgaggaagatttgctgtgagtgatttgatgagacaga 655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 866 tccacgaggaagcagatgctgtgtactctatagagccacccagcttgcaactgaatca 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 656 acacctttcgaacatgctgtgtgtactctatagagccgcctgaggttgctctgcatgta 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 926 cgacagctctgtacaaattctgtaacagcagttgtgtgagggagtgaaaccgcgcgc 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 716 ccaaccatccactacaactacatgtagtaaacagttccgactggtgagcagacaggaagc 775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 986 caatttaactcatgttactctggaacacagatgaggaatcctctggtgcagcgtct 1045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 776 ccattctccatcatcacatcagatcagatccagttgtaattacttgaggaacagatc 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1046 ttgagggccgagtcgtgtgttggccaggaagagacaggaagcggttgtagatagcata 1105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 836 ttgaggtgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1106 gaagaagagaagtttcgagacatcaaaagaacggtgtagtgcagccgcttgcgc 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 896 ggaagaagggagagctccacagcgtctcccccagggagcactaagcagacatgccc 955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1166 agaacaacacatggtatccagatgacatcaacaaagaacgaagatccccaatgtagaac 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 956 acaaacac-----cagctcctctcccaagcaaaagaagaacacatgtagtagaat 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1226 tgttacttaccagtgagggcggtgagactatgaatgtgttgtagatcaagaagt 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1007 attcaacctttagacggcggtgagcgtcttcgaaatgttcgagagcgtcaatgag 1066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1286 cccctggaactcatgtagtactcctccagca 1316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1067 ccttgaactcaagatgcccagcgttgga 1097
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

SCREEN: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15353
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/431,357
FILING DATE: 28-APR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/456,623
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: W5158CPT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-15353-20

```

```

Query Match      8.7%; Score 244.2; DB 5; Length 1215;
Best Local Similarity 58.3%; Pred. No. 6.4e-59;
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 506 ctccatccacgcgcacatccctcccaaacgcagaccagccgcagcagtttcagcgt 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 302 CCTGTCACTTCTGTCTCCCTTCCGAAACCTACACAGGCGACGTTCCTCTGG 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 566 ccttcagcagtcgagcagccagtcgcccagtcgagctatccactgaactgaaga 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 362 GCTTCTTGCACTTGTGGAGACGCAAGCTGTGACTTGCACTACTCCCTGCTCAACA 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 626 aactctactgccaacttgcaagacatgcccattccagatcaagtgatgacccacc 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 422 AGATGTTTGGCAACTGTGGAGAACCTGCTGTCACACTGTGGGTGATTCCACACCCC 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 686 ctcaagggagcgtgtatccgcgcacatgctcgtctacaaaaagctgagcagtgagg 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 482 GCGCCGGAACCGCGCTCGCGCCATGCGCATCTACACACACTACACACATGAGAGG 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 746 tggtagagcggtgcccacacatgagctgagccgtgtaattcaacgagggacagattgcc 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 542 TTGTGAGGCGCTGCCCCACCATGAGCGCTGCTCAGATAGCGATG-----GTCGAGCC 595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 806 ctctcagtcatttgatcgagtagagggagcaacgacatgcccaglatgtagaagatccca 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 596 CTCTCACACATCTTATCCGAGTGAAGGAATTGCGGTGAGATTTGGATACAGAA 655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 866 tcaacgaggaagcagatgctgtgtgtactctatgagccacccagcttgagcagtaatca 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 656 ACACCTTTGACATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 926 cgacagctcttatacatctatgcttaacagcagttgtgtgagggagtagaacgcgcgc 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



```

Db 716 CCACATCCACATACATACATGTGTACAGTCTCTGCATGGCGCGCATGAACCGAGGC 775
Qy 986 caatttaatacttctgtctctgtgaaccagaagatggtgacgctgtct 1045
Db 776 CCATCCTCACCATCATCATCTGCAAGACTCCAGTGTAACTACTGTGGACCGAACACT 835
Qy 1046 ttgaagcccgatctgtctgtcccgagaagaagacgagcgatgaagatagcatca 1105
Db 836 TTGAGGTGCGGTGTGTGTCTCTCTGCGAGAGACCGCGCACAGAGAAAGAAATCTTC 895
Qy 1106 gaaagcagcaagttctgcagcagtlacaagaacggtgagtgatgagagccgcttctc 1165
Db 896 GCAAGAAAGGAGGAGGCTCACCACAGAGTCCCGCCAGGGAGCACTAAGGAGACCTGCCCA 955
Qy 1166 agaacacacatggtatccagatgacatccatcaagaagaatccccagatgtgaac 1225
Db 956 ACAACAC-----CAGCTCTCTCTCCCAAGCCAAAGAAACCACTGTGATGAGAAAT 1006
Qy 1226 tgtatactaccagtgagggcgctgagactatgaaatgctgttgaagatcaagaagt 1285
Db 1007 ATTTCACCTTCATCATCTCGCGGCGCTGAGCGCTTGAAATGTTCGAGAGCTGAATGAGG 1066
Qy 1286 ccctggaaactcagtgagctctcctcagca 1316
Db 1067 CCTTGAACTCAAGAGATGCCCAAGCTGGGAA 1097

```

```

RESULT 6
US-08-486-663A-18
; Sequence 18, Application US/08486663A
; Patent No. 5968761
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume Cottarel
TITLE OF INVENTION: Ubiquitin Conjugating Enzymes
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,663A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-029CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

```

```

; NAME/KEY: CDS
; LOCATION: 1..1182
US-08-486-663A-18

```

```

Query Match      8.6%; Score 242.6; DB 2; Length 1181;
Best Local Similarity 58.2%; Pred. No. 1.8e-58;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

```

```

Qy 506 ctcatcaccgcgcattccctccaaacacgcgactaccagcgccgcagatlttgcagtg 565
Db 275 CCCTGTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 334
Qy 566 ccttcagcagtcgagcagccgagctgagccagcttgagcagcttcaactaaactgaaga 625
Db 335 GCTTCTTGATTTGTGGAGACGCAAGCTGTGATGCTTGACGCTTCTCTCTCTCTCTCTCT 394
Qy 626 aactctactgccaatltcaagaacatgcccatccatccagatcaagtgatgaaccacctc 685
Db 395 AGATGTTTTGCCAATCGGCAAGACCTGCCCTGTGACAGCTGTGATTCACACGCC 454
Qy 686 ctcaaggagctgttataccgcgcattgctgtctacaagaacgctgagcagctcagagag 745
Db 455 CGCCCGGACCCGCGCTCCGCGCATGCGCATCTTACAAACAGTACAGGACATGACGAGAG 514
Qy 746 tggtaagcgggtgcccccaacatgagctgagcggtaattcaacgaaggagacagattggc 805
Db 515 TTGTAGGCGCTGCCCCCAACCATGAGCCCTGCTCAGATAGCATG-----GTCGTGGCC 568
Qy 806 ctctcagtcatttgaattcagagtagagggaaacagccatgcccagatglagaagatccca 865
Db 569 CTCCTCAGACTTATTCGAGATGGAAGAAATTTGCGTGTGAGATTTGGATGACAGAA 628
Qy 866 tcaagaagaacagagtgctgtgtacattatgagccacccaggtgtgacatgaattca 925
Db 629 ACACCTTTTCGACATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 688
Qy 926 gcaagcttgtagcaattcatatglttaacagagctgtgtgtgtgtgtgtgtgtgtgtgt 985
Db 689 CCACCATCCTACATCACTACATGATGTAACTGCTGCATGTGGCGCATGAACCGGAGGC 748
Qy 986 caatttaatacttctgtctctgtgaaccagaagatggtgacgctgtct 1045
Db 749 CCATCCTCACCATCATCATCTGCAAGACTCCAGTGTAACTACTGTGGAGCGAACAGCT 808
Qy 1046 ttgaagcccgagatctgtgtctgtccagagaagacaggaagcggtgtgaagatagcatca 1105
Db 809 TTGAGGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 868
Qy 1106 gaaagcagcaagttctgcagcagtlacaagaacggtgagtgatgtagagagccgcttctc 1165
Db 869 GCAAGAAAGGAGGAGGCTCACCACAGAGTCCCGCCAGGGAGCTAAGGAGAGTGTGCCCA 928
Qy 1166 agaacacacatggtatccagatgacatccatcaagaagaatccccagatgtgaac 1225
Db 929 ACAACAC-----CAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 979
Qy 1226 tgtatactaccagtgagggcgctgagactatgaaatgctgttgaagatcaagaagt 1285
Db 980 ATTTCACCTTCATCATCTCGCGGCGCTGAGCGCTTGAGATGTTCGAGAGCTGAATGAGG 1039
Qy 1286 ccctggaaactcagtgagctctcctcagca 1316
Db 1040 CCTTGAACTCAAGAGATGCCCAAGCTGGGAA 1070

```

```

RESULT 7
US-08-247-904B-11
; Sequence 11, Application US/08247904B
; Patent No. 5981699
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.

```

```

APPLICANT: Draetta, Giulio
TITLE OF INVENTION: Human Upliquitin Conjugating Enzyme
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,904B
FILING DATE: 23-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-7000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1181
US-08-247-904B-11

```

```

Query Match      8.6%; Score 242.6; DB 2; Length 1181;
Best Local Similarity 58.2%; Pred. No. 1.8e-58;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

QY 506 ctccacacccgcatccctcccaaacacgactaccacagcccgccgacgttccgacgt 565
DB 275 CCTCTGATCTCTGTCCTTCCACAAAACCTACACAGGCGACTACGCTTCCGCTGG 334
QY 566 ccttcacagctcgagacacgcaagtcgcaacctgagcgtattccactgaactgaaga 625
DB 335 GCTTCTTGATCTGGGACAGCCAACTGTGTGACTTGACACTACCTACCTCCCTGCTCA 394
QY 626 aactctactgcgaattgcaagacacatgcacatcagaatcgaagtgtgacccactc 685
DB 395 AGATGTTTTCACAACTGGCCAAAGACCTGCTGCTGACCTGTGGGTTTATTCACACCCC 454
QY 686 ctcaaggagctgtatccgacgcatgctgttataaaaagctgagacgtcacgagag 745
DB 455 CGCCGGGACACCGCGCTCCGCCATGCGCATCTACAACTACAGACATGACGAGAGG 514
QY 746 tggtagaagtggtgcccacacatgagctgagcgtgaaattcaagagagagacgttccc 805
DB 515 TTGTGAGGGGCTGCCCCACCATGAGCGCTGCTGAGATGAGGATG-----GCTGAGCC 568
QY 806 ctccagtagatgtatcgagtagaggggaaacacacatgcccagtagtagaagatccca 865
DB 569 CTCCTCAGCATCTTATCGAGTGGAGAAATTTGCGTGTGGAGATATTGATGACGAA 628
QY 866 tcaagagagagagagtgctgtgtactatgagccacccacaggttgagcagaattca 925
DB 629 ACACCTTTGACATAGTGTGTGTGCTATATGAGCCGCTGAGGTGGTCTGACTGTA 688
QY 926 cgacagctctgtacatctatgtgtacacagcgttggtgtgagagatgaacgcgcgc 985

```

```

DB 689 CCACATCCACTACACTACATGTGTAAACAGTTCTGTGATGGCGGCAGTAAACCGGAGC 748
QY 986 caatttaatcatgttactcttgaaacacagagatgaggaaicctcgtggccgacgtcgt 1045
DB 749 CCATCTCAGCATCATATACACTGGAAGACTCCAGTGTGTATCTACTGGAGGAGACACT 808
QY 1046 ttgagcccgagctgtgtgttcccaagaaagacagaaagcgagtagatgacatca 1105
DB 809 TTGAGGTGCTGTGTGTGTGCTGTGCGGAGAGACCGCGCCACAGAGAAAGATCTCC 868
QY 1106 gaaagcagcaggttcgagcagtagaagaagacggtgagtagaagagcccggttcgtc 1165
DB 869 GCAAGAAAGGGAGGAGCCTCACACAGACTGCCCCAGGAGGACACTAAGGAGACACTGCCA 928
QY 1166 agaacacacatgtatccagatgacatccatcaagaagaagatccccagatgataac 1225
DB 929 ACACAC-----CAGCTCTCTCCACGCAAGCAAGAAACCACTGATGAGAAAT 979
QY 1226 tgttacttaccagtgagggcggtgagacttgaatgctgttgaagatcaagaagt 1285
DB 980 ATTTCACCTTACATCCGTGGGCGGTGAGCGCTTCGAGATGTTCCGAGACTGATAGAG 1039
QY 1286 cccctgaaactcatgacgtaccttcctcagca 1316
DB 1040 CCTGGAACCTCAAGAGATGCCAGGCTGGGAA 1070

```

```

RESULT      8
US-08-767-942A-22
Sequence 22, Application US/08/67942A
Patent No. 6068982
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Chiu, M. Isabel
APPLICANT: Berlin, Vivian
APPLICANT: Damagnez, Veronique
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1179
US-08-767-942A-22

```





Patent No. 5843654  
GENERAL INFORMATION:  
APPLICANT: DAHLBERG, JAMES E.  
APPLICANT: LYAMICHEV, VICTOR I.  
APPLICANT: BROW, MARY ANN D.  
APPLICANT: OLDENBURG, MARY C.  
APPLICANT: HEISLER, LAURA  
TITLE OF INVENTION: DETECTION OF p53 MUTATIONS  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,956  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/402,601  
FILING DATE: 09-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,164  
FILING DATE: 09-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/254,359  
FILING DATE: 06-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,384  
FILING DATE: 04-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/986,330  
FILING DATE: 07-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL J., PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01801  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1182 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-484-956-94

Query Match 8.6%; Score 242.6; DB 2; Length 1182;  
Best Local Similarity 58.2%; Pred. No. 1.8e-58;  
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;  
QY 506 ctcacatccgcgcacatccctcccaaacacgactaccacgagcccgacagtttcgaagt 565  
DB 275 cccctgacatcttctgtgcttccacagaaacacgacgagcctgacggttccgctcg 334  
QY 566 ccttcaagcagtcgagcaccgacgaagtcggcaacctgacgtatcttcacatgacgaaga 625  
DB 335 gcttcttgcatcttgagacacgcaactctgtgacttgacacgtracctccctgcccttaaca 394  
QY 626 aactctactgcaaatgtcaagaacatgcccatccacatcagaatgagtgatgacccaccc 685  
DB 395 agatgtttggcacaactggcgaagacctgctgtgcagctgtgggttgattccacaccc 454

QY 686 ctcaggaagctgtatccgcgcacatcgctctacaanaagctgagcagtcacgagag 745  
DB 455 cgcgcgcgcacacccgcgctccgcgcatcgatccatctacagacagtcacacgacatgacgag 514  
QY 746 tggtagagcgtgtgcccacacatgagctgagccgtgaattcaacgagggacagatgcc 805  
DB 515 ttgtgagggcgctgccccccacacatgacgctgctgacatgacgagcagc-----ctgtggccc 568  
QY 806 ctcctagatatttgatagtagtagagggagacacgacatgcccagatgtagaagatccca 865  
DB 569 ctcttcagatcttattacccagtgaggaagaaatttgctgtagagttttgtagatgacagaa 628  
QY 866 tcacagaagacagagtgctgctgtagcctatgagccaccagtgctgacatgacaa 925  
DB 629 acacttttgacatagctggtggtgctccctatgagcgcgctgaggtggctctgactgta 688  
QY 926 cgacagcttgtagacaattcattgtgtaacagagtggtgtggaaggatgaaacgcgcgc 985  
DB 689 ccacacatccactaacatgacatgacacgacgagacgctgacgagcgcgacgagac 748  
QY 986 caatttaactatgttactctggaacacagagatgaggaagtcctggcgagcagctgt 1045  
DB 749 ccattctcaccatcactacacacgacgagacgctgacgagacgagacgagacgagacgct 808  
QY 1046 ttgaagcccgagctgtgcttcccagagaagacagagagcgagtgagatagacatca 1105  
DB 809 ttgaggtgctgtgttggcttctctggagagacccggccacagaggaagaaatctcc 868  
QY 1106 gaagaacagaagtttcgacgacatacaagaacggtgatgtgacgagcgcggttgcgc 1165  
DB 869 gcaagaaaggagagcgtcaccacacgacgctccccacgagacacgactaagacagacgaccca 928  
QY 1166 agaacacacatgtagtccagatgacatccatcaagaacgaagatccacagatgtagaac 1225  
DB 929 acacacac-----cagctccttcccacgacaaagaaacccatgtagagaaat 979  
QY 1226 tgtatactaccagtgagggccgtgagacattatgaatgctgtgtagaagacaagaat 1285  
DB 980 atttacccttccatgacgtcgtggcgtgagcgccttgcagatgttccagacgactgaatgagc 1039  
QY 1286 ccctggaactatgacagatccctccacga 1316  
DB 1040 ccttggaactcaagatgccacgagcgtgggaa 1070

RESULT 12  
US-08-757-653-92  
Sequence 92, Application US/08757653  
Patent No. 5843659  
GENERAL INFORMATION:  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Lyamichev, Natasha  
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,653  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.  
 REGISTRATION NUMBER: 40,027  
 REFERENCE/DOCKET NUMBER: FORS-02565  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-8410  
 TELEFAX: (415) 397-8338  
 INFORMATION FOR SEQ ID NO: 92:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1182 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-757-653-92

Query Match 8.6%; Score 242.6; DB 2; Length 1182;  
 Best Local Similarity 58.2%; Pred. No. 1.8e-58;

Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

```

QY 506 ctccatcacccgcacatccctcccaacacgacacccagccgacagttcgagcgt 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 CCCTGTCATCTTCTGTCCTTCCAGAAAACCTACAGGCGAGTTCGCTGG 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 566 cctccagcagtgagacagccgacagtcgagccacgtgacgtattccactgaactgaaga 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 GCTTCTTGCACTTGTGGAGACGCCAAGTCTGTGACTTGACAGTACCTCCCTGCGCTCAACA 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 626 aactctactgcgaatctgcaaaagacatgcgccatccagatcaagtgatgacccaccc 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 AGATGTTTGGCAACTGCGCAAGACGTGCCCTGTGCGAGCTGTGGTTGATTCACACCCC 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 686 ctgagagagctgtatccgcgcacatgcctctcaaaaaagctgagcagtcagagag 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 CGCCCGGACCCCGCTCCGCGCATGCGCATACAAAGTACAGACATGACAGGAG 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 746 tgggtgaagcgtgcccccaacatgagctgagcgtgaattcaacgagagagatgccc 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 TTGTGAGGCGCTGCCCCACATGAGCGCTGCTCAAGTACGATG-----GTCTGGCCC 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 806 ctctcagtcatttgatcagtagagagagagacagccatgccagtagtagaagatccca 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 569 CTCTCTGACATCTTATCCGATGGAAGAAATTGGCGTGGAGTATTGGATGACAGAA 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 866 tcaacaggaagacagagtggtgctgttccctatgagccacccaggttgcagtaattca 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 629 ACACCTTTGACATTAAGTGTGTGCTCCCTATGAGCGCGCTGAGGTTGCTCTGACTGTA 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 926 cgaagctctgtacaattcaatgtgtaacagcagtggtgtgagagagatgaacccgctgc 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 689 CCACCATTCCTCACTCACTACATGTGTACAGATTCCTGCGATGGCGGCGATGAACCGGAGGC 748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 986 caatttaactctgttactctggaacacagagatgaggcaagtcctgagcgacgctgct 1045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 749 CCATCTCTCACTCACTCACTCACTGAGACTCCAGTGCTAATCTACTGAGGAGCGAACAGCT 808
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1046 ttgaagcccgagatctgtgcttccaggaagagacagagagcgagtagaagatagcatca 1105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 809 TTGAGGTGGGTGTGTGTGCTCTCCCTGGGAGAGACCGCGCCACAGAGAGGAATTCCTC 868
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1106 gaaagcagcagatcttcgagcagtagaagaagacggtgtagtgcagagccgcttctc 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 869 GCAGAGAAAGGGAGGCTCCACACAGAGCTGCCCGCAGGAGGACTAAGAGAGACACTGCCCA 928
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1166 aagaacacatgtagtcaagatgacatcacaagaagaacggaagatccacagatgagaac 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 929 ACAACAC-----CAGCTCTCTCCCAAGCCAAAGAAACACATGATGAGGAAAT 979
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1226 tttataacttaccagtgagagcgctgagagactatgaaatgctgttgaagatcaagaagt 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 980 ATTTCACCTTCAGATCGGTGGGCGGTGAGCCCTTCGAGATTTCCGAGAGCTGAATGAGG 1039
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1286 cccttgaagactatgtagtaccttccacaga 1316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 1040 CCTTGAACCTCAGAGATGCGCCAGCTGGGAA 1070

# RESULT 13

US-08-757-653-94  
 ; Sequence 94, Application US/08757653  
 ; Patent No. 5843669  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaiser, Michael W.  
 ; APPLICANT: Lyamichev, Victor I.  
 ; APPLICANT: Lyamichev, Natasha  
 ; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
 ; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases  
 ; NUMBER OF SEQUENCES: 190  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Medlen & Carroll, LLP  
 ; STREET: 220 Montgomery Street, Suite 2200  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States Of America  
 ; ZIP: 94104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/757,653  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ingolia, Diane E.  
 ; REGISTRATION NUMBER: 40,027  
 ; REFERENCE/DOCKET NUMBER: FORS-02565  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 705-8410  
 ; TELEFAX: (415) 397-8338  
 ; INFORMATION FOR SEQ ID NO: 94:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1182 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-757-653-94

Query Match 8.6%; Score 242.6; DB 2; Length 1182;  
 Best Local Similarity 58.2%; Pred. No. 1.8e-58;  
 Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

```

QY 506 ctccatcacccgcacatccctcccaacacgacacccagccgacagttcgagcgt 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 CCCTGTCATCTTCTGTCCTTCCAGAAAACCTACAGGCGAGTTCGCTGG 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 566 cctccagcagtgagacagccgacagtcgagccacgtgacgtattccactgaactgaaga 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 GCTTCTTGCACTTGTGGAGACGCCAAGTCTGTGACTTGACAGTACCTCCCTGCGCTCAACA 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 626 aactctactgcgaatctgcaaaagacatgcgccatccagatcaagtgatgacccaccc 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 AGATGTTTGGCAACTGCGCAAGACGTGCCCTGTGCGAGCTGTGGTTGATTCACACCCC 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 686 ctgagagagctgtatccgcgcacatgcctctcaaaaaagctgagcagtcagagag 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 CGCCCGGACCCCGCTCCGCGCATGCGCATACAAAGTACAGACATGACAGGAGGAG 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 746 tgggtgaagcgtgcccccaacatgagctgagcgtgaattcaacgagagagatgccc 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 TTGTGAGGCGCTGCCCCACATGAGCGCTGCTCAAGTATGCGATG-----GTCTGGCCC 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 806 ctctcagtcatttgatcagtagagagagagacagccatgcccagtagtagaagatccca 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db      569 CTCCACGACATCTTATCCGAGCTGCAAGAAATTTCGCTGTGAGATTTGGATGACACAGAA 628
Qy      866 tcaacaggaagacagagtgctgtgtactatgtgacccaccccaagttgacactgaatca 925
Db      629 ACATCTTTCGACATGATGTGGTGGCCCTTATGAGCCCTGAGGTGGCTCTGACTGTGA 688
Qy      926 cgaacagctgttacaattcatgtgtacacagagtgctgtgtggaaggaatgaacccgctc 985
Db      689 CCACCATTCACATACACATACATGCTGTACAGTTCCTGCATGGCGCGCATGAAACCGGAGAC 748
Qy      986 caatttaacatctgttactctgtgaaacacagagatgaggaagctcctgggcccgaagctgt 1045
Db      749 CCATCCTCACCATCATCATCACTGGAAGACCTCCAGTGTAACTACTATGTGGAGGAGAACACT 808
Qy      1046 ttgagcccgagatctgtgtctgtgcccagaagaagacaggaagcgagatgaatagatca 1105
Db      809 TTGAGGTGCTGTGTGTGCTGTGCTGTGGAGAGACCGCGCACAGAGAGAGAAATCTCC 868
Qy      1106 gaaagcagcaagtttcgagacagtaacaagaagcggtgagatgagcagccgcttctgtc 1165
Db      869 GCAAGAAAGGGAGGAGCTTCACACAGAGCTGCCCCAGGAGACATGAGGAGACTGCCCCA 928
Qy      1166 agaacacacatgtaatacagatgacatccatcaagaagaagatccacagatgagac 1225
Db      929 ACAACAC-----CAGCTCTCTCCCAAGCCCAAGAAAGAACCACTGATGAGAAAT 979
Qy      1226 tgtataacttaccagtgagggcggtgagactatgaatgtctgttgaagatcaagaagt 1285
Db      980 ATTTCACCTTCAGATCCGTGGGCGCTGAGCGCTTCGAGATGTTCGAGAGCTGAAATGAGG 1039
Qy      1286 cccctgaactcatgcaagtaacttccctcagca 1316
Db      1040 CCTTGAACTCAAGATGCCAGGCTGGGAA 1070

```

## RESULT 14

US-08-458-356-215

Sequence 215, Application US/08458356

Patent No. 5942235

GENERAL INFORMATION:

APPLICANT: Paolletti, Enzo

APPLICANT: Tartaglia, James

APPLICANT: Cox, William J.

TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY

NUMBER OF SEQUENCES: 217

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris &amp; Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

```

; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-458-356-215

Query Match      8.6%, Score 242.6; DB-2; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1,86-58;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

```

```

Qy      506 ctcaatcaccgcatccctcccaacaccgactaccagcccgacagtttgaagcgt 565
Db      275 CCGTGTCAATCTTGTCTCCCTCCAGAAACCTTACAGGGAGCTTACGTTCCCTGTGG 334
Qy      566 ccttcacagcagtcgaaacccgagtcgcccacttgacgtatccactgaactgaaga 625
Db      335 GCTTCTTCATTTCTGGGACAGCCAGCATGCTGTGACTTGCACGTACTCCCTGCCCTCAACA 394
Qy      626 aactctactgcnaatttgcaagaacatgcccacatccagatcaaggatgaagccaccc 685
Db      395 AGATGTTTGGCAACTGGGCAAGACCTGCCCTGTGCTGACGTGTGGTTGATTCACACACCC 454
Qy      686 ctcaaggagctgttataccgagcactgtctctcaaaaaagctgagcagctcaagag 745
Db      455 CGCCCGGACCCGCGCTCCGCGCATGGCCATCTAACACAGTCACAGCATGACGAGG 514
Qy      746 tggtaagcgggtgcccacaaatgagctgagcgtgaaatcaagagagacagatgtcc 805
Db      515 TTGTAGGGCGCTGCCCCACCACTGAGCGCTGTGATGATGAGCAT-----CTGTGGCC 568
Qy      806 ctccatgaatctgtatctgagtagaaggagacagccatgcccagatgtaagaatccca 865
Db      569 CTCCACGACATCTTATCCGAGTGAAGAAATTTCGCTGTGAGATTTGGATGACACAGAA 628
Qy      866 tcaacaggaagacagagtgctgtgtactatgtgacccaccccaagttgacactgaatca 925
Db      629 ACATCTTTCGACATGATGTGGTGGCCCTTATGAGCCCTGAGGTGGCTCTGACTGTGA 688
Qy      926 cgaacagctgttacaattcatgtgtacacagagtgctgtgtggaaggaatgaacccgctc 985
Db      689 CCACCATTCACATACACATACATGCTGTACAGTTCCTGCATGGCGCGCATGAAACCGGAGG 748
Qy      986 caatttaacatctgttactctgtgaaacacagagatgaggaagctcctgggcccgaagctgt 1045
Db      749 CCATCCTCACCATCATCATCACTGGAAGACCTCCAGTGTAACTACTATGTGGAGGAGAACACT 808
Qy      1046 ttgagcccgagatctgtgtctgtgcccagaagaagacaggaagcgagatgaatagatca 1105
Db      809 TTGAGGTGCTGTGTGTGCTGTGCTGTGGAGAGACCGCGCACAGAGAGAGAAATCTCC 868
Qy      1106 gaaagcagcaagtttcgagacagtaacaagaagcggtgagatgagcagccgcttctgtc 1165
Db      869 GCAAGAAAGGGAGGAGCTTCACACAGAGCTGCCCCAGGAGACATGAGGAGACTGCCCCA 928
Qy      1166 agaacacacatgtaatacagatgacatccatcaagaagaagatccacagatgagac 1225
Db      929 ACAACAC-----CAGCTCTCTCCCAAGCCCAAGAAAGAACCACTGATGAGAAAT 979
Qy      1226 tgtataacttaccagtgagggcggtgagactatgaatgtctgttgaagatcaagaagt 1285
Db      980 ATTTCACCTTCAGATCCGTGGGCGCTGAGCGCTTCGAGATGTTCGAGAGCTGAAATGAGG 1039
Qy      1286 cccctgaactcatgcaagtaacttccctcagca 1316
Db      1040 CCTTGAACTCAAGATGCCAGGCTGGGAA 1070

```

## RESULT 15

US-08-796-101-46

```

; Sequence 46, Application US/08796101
; Patent No. 6183752
; GENERAL INFORMATION:
; APPLICANT: EPSTEIN, STEPHEN E.
; APPLICANT: FINKEL, TOREN
; APPLICANT: SPEIR, EDITH
; APPLICANT: ZHOU, YI FU
; APPLICANT: ZHU, JIANHUI
; APPLICANT: BRIDLE, LORNE
; APPLICANT: PINCUS, STEVEN
; TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
; TITLE OF INVENTION: PROPHYLAXIS AND THERAPY
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESS: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: KOMALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 764-5574
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-796-101-46

```

```

Query Match      8.6%; Score 242.6; DB 4; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1.8e-58;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

```

```

QY 506 ctccatccagccgcatccctccgaacacccagccagccgacagcttccgacgtgt 565
DB 275 CCCGTCATCTTGTGCTCCCTCCAGAAACCTACCAAGGCGACGTACGGTTCCGCTGG 334
QY 566 cctccagcagctcgagacccgcaagtcgagccacctgagcgtatctccactgaactgaaga 625
DB 335 GCTTCTTGCAATTCGGAGACGCAAGCTGTGACTTGACGTACTCCCTCCCTCAACA 394
QY 626 aactctactgccaatctgaagaagacatgcccctccagatccaagtgtgatacccccacctc 685
DB 395 AGATGTTTGCACAACTGGCCAGACCTGCTGTCAGCTGTGGGTTGATTCCACACCCC 454
QY 686 ctccaggaagctgtatccgagcccatgctctacaaaaaagctgagcaagctgacgagag 745
DB 455 CGCCCGGACACCGCGGTCCGGCCATGSCCATCTACAAAGCAGTCACAGCAGCATGACGGAGG 514
QY 746 tggtagaagcggtgcccacacatgagctgagcggtgaattcaacgagaggaagattggccc 805
DB 515 TTGAGAGCGCTGCCCCACCATGAGCGCTGCTCAGATAGCGATG-----GTTGCGCC 568
QY 806 ctccatgacttggatccgagtagagaggaacagccatgcccagtagtagaagatccca 865
DB 569 CTCTCAGACATCTTATCCGAGTAGGAGAAATTGGCTGTGAGATTATTGGATGACAGAA 628

```

```

QY 866 tccaggaagacagagtgctgtgtacttaagagccaccocccaggttggcactgaattca 925
DB 629 ACACTTTTCGACATATGAGTGTGTGCTCCTATAGCCGCTGAGGTGGCTCTGATGTGA 688
QY 926 cgaagctctgtacaatttcaattgtlaaacagcagttgttggaggatgaaccgctgc 985
DB 689 CCACCATCCCACTACACTACATGATGTAAAGTCTTCGATGGCGGCATGAAACCGGAGGC 748
QY 986 caatttaacatgttactctgtgaacacagagatgaggcaagtcctgggcccagcgtgct 1045
DB 749 CCATCTCTACCATCATCATCATCTGGAAGACTCCAGTGGTAATCTACTGGGACGACAGCT 808
QY 1046 ttgagcccgatcgtgtcttgcaggaagagacaggaagcgga tgaagatagcatca 1105
DB 809 TTGAGTGCGGTGTGTGCTGCTGCTGAGAGACGCGCCACAGAGGAAGAGAAATCTCC 868
QY 1106 gaaagcagcaagtttcgagacgtacaaagaacggtgtatgttaccgaagcgccgttcgctc 1165
DB 869 GCAAGAAAGGGAGCCTACACACAGAGCTGCCCCAGGAGACACTAAGCCGACACTGCCCA 928
QY 1166 agaacacacatggtatccagatgacatccatcaagaagaagatccccagatgataaac 1225
DB 929 ACAACAC-----CAGCTCTCTCCCAAGCCAAAGAAAGAACCTGTGATGGAGAAAT 979
QY 1226 tgtatacttaccagtgagggccgtgagacttatagaatgctgttgaagatcaaaagat 1285
DB 980 ATTTCACCCCTTCACATCCGTGGGCGGTGAGGCGCTTCGAGATGTTCCGAGACTGGAATGAGG 1039
QY 1286 cccttgaactatgacgtactcctcaagca 1316
DB 1040 CTTGGAACCTCAAGATGCCCAAGCTGGGAA 1070

```

Search completed: August 8, 2001, 00:15:37  
Job time: 10243 sec





**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2001, 20:37:04 ; Search time 2712.11 Seconds  
(without alignments)  
9814.954 Million cell updates/sec

Title: US-09-670-568b-2  
Perfect score: 2816  
Sequence: 1 tcgtgatacaagaacagt.....gcatttggttaaagaaa 2816

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1022815 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est25:\*  
26: gb\_est26:\*  
27: gb\_est27:\*  
28: gb\_est28:\*  
29: gb\_est29:\*  
30: gb\_est30:\*  
31: gb\_est31:\*  
32: gb\_est32:\*  
33: gb\_est33:\*  
34: gb\_est34:\*  
35: gb\_est35:\*  
36: gb\_est36:\*  
37: gb\_est37:\*  
38: gb\_est38:\*  
39: gb\_est39:\*  
40: gb\_est40:\*  
41: gb\_est41:\*  
42: gb\_est42:\*  
43: gb\_est43:\*  
44: gb\_est44:\*  
45: gb\_est45:\*  
46: gb\_est46:\*  
47: gb\_est47:\*  
48: gb\_est48:\*  
49: gb\_est49:\*  
50: gb\_est50:\*  
51: gb\_est51:\*  
52: gb\_est52:\*  
53: gb\_est53:\*  
54: gb\_est54:\*  
55: gb\_est55:\*  
56: gb\_est56:\*  
57: gb\_est57:\*  
58: gb\_est58:\*  
59: gb\_est59:\*  
60: gb\_est60:\*  
61: gb\_est61:\*  
62: gb\_est62:\*  
63: gb\_est63:\*  
64: gb\_est64:\*  
65: gb\_est65:\*  
66: gb\_est66:\*  
67: gb\_est67:\*  
68: gb\_est68:\*  
69: gb\_est69:\*  
70: gb\_est70:\*  
71: gb\_est71:\*  
72: gb\_est72:\*  
73: gb\_est73:\*  
74: gb\_est74:\*  
75: gb\_est75:\*  
76: gb\_est76:\*  
77: gb\_est77:\*  
78: gb\_est78:\*  
79: gb\_est79:\*  
80: gb\_est80:\*  
81: gb\_est81:\*  
82: gb\_est82:\*  
83: gb\_est83:\*  
84: gb\_est84:\*  
85: gb\_est85:\*  
86: gb\_est86:\*  
87: gb\_est87:\*  
88: gb\_est88:\*  
89: gb\_est89:\*  
90: gb\_est90:\*  
91: gb\_est91:\*  
92: gb\_est92:\*  
93: gb\_est93:\*  
94: gb\_est94:\*  
95: gb\_est95:\*  
96: gb\_est96:\*  
97: gb\_est97:\*  
98: gb\_est98:\*  
99: gb\_est99:\*  
100: gb\_est100:\*  
101: gb\_est101:\*  
102: gb\_est102:\*  
103: gb\_est103:\*  
104: gb\_est104:\*  
105: gb\_est105:\*  
106: gb\_est106:\*  
107: gb\_est107:\*  
108: gb\_est108:\*  
109: gb\_est109:\*  
110: gb\_est110:\*  
111: gb\_est111:\*  
112: gb\_est112:\*  
113: gb\_est113:\*  
114: gb\_est114:\*  
115: gb\_est115:\*  
116: gb\_est116:\*

44: em\_esthum10:\*  
45: em\_esthum11:\*  
46: em\_esthum12:\*  
47: em\_esthum13:\*  
48: em\_esthum14:\*  
49: em\_esthum15:\*  
50: em\_esthum16:\*  
51: em\_esthum17:\*  
52: em\_esthum18:\*  
53: em\_esthum19:\*  
54: em\_esthum20:\*  
55: em\_esthum21:\*  
56: em\_esthum22:\*  
57: em\_esthum23:\*  
58: em\_esthum24:\*  
59: em\_esthum25:\*  
60: em\_esthum26:\*  
61: em\_esthum27:\*  
62: em\_esthum28:\*  
63: em\_esthum29:\*  
64: em\_esthum30:\*  
65: em\_esthum31:\*  
66: em\_esthum32:\*  
67: em\_esthum33:\*  
68: em\_esthum34:\*  
69: em\_esthum35:\*  
70: em\_esthum36:\*  
71: em\_esthum37:\*  
72: em\_esthum38:\*  
73: em\_esthum39:\*  
74: em\_esthum40:\*  
75: em\_esthum41:\*  
76: em\_esthum42:\*  
77: em\_esthum43:\*  
78: em\_esthum44:\*  
79: em\_esthum45:\*  
80: em\_esthum46:\*  
81: em\_esthum47:\*  
82: em\_esthum48:\*  
83: em\_esthum49:\*  
84: em\_esthum50:\*  
85: em\_esthum51:\*  
86: em\_esthum52:\*  
87: em\_esthum53:\*  
88: em\_esthum54:\*  
89: em\_esthum55:\*  
90: em\_esthum56:\*  
91: em\_esthum57:\*  
92: em\_esthum58:\*  
93: em\_esthum59:\*  
94: em\_esthum60:\*  
95: em\_esthum61:\*  
96: em\_esthum62:\*  
97: em\_esthum63:\*  
98: em\_esthum64:\*  
99: em\_esthum65:\*  
100: em\_esthum66:\*  
101: em\_esthum67:\*  
102: em\_esthum68:\*  
103: em\_esthum69:\*  
104: em\_esthum70:\*  
105: em\_esthum71:\*  
106: em\_esthum72:\*  
107: em\_esthum73:\*  
108: em\_esthum74:\*  
109: em\_esthum75:\*  
110: em\_esthum76:\*  
111: em\_esthum77:\*  
112: em\_esthum78:\*  
113: em\_esthum79:\*  
114: em\_esthum80:\*  
115: em\_esthum81:\*  
116: em\_esthum82:\*

```
117: gb_est148:*
118: gb_est149:*
119: gb_est150:*
120: gb_est151:*
121: gb_est152:*
122: gb_est153:*
123: gb_est154:*
124: gb_est155:*
125: gb_est156:*
126: gb_est157:*
127: gb_est158:*
128: gb_est159:*
129: gb_est160:*
130: gb_est161:*
131: gb_est162:*
132: gb_est163:*
133: gb_est164:*
134: gb_est165:*
135: gb_est166:*
136: gb_est167:*
137: gb_est168:*
138: gb_est169:*
139: gb_est170:*
140: gb_est171:*
141: gb_est172:*
142: gb_est173:*
143: gb_est174:*
144: gb_est175:*
145: gb_est176:*
146: gb_est177:*
147: gb_est178:*
148: gb_est179:*
149: gb_est180:*
150: gb_est181:*
151: gb_est182:*
152: gb_est183:*
153: gb_est184:*
154: gb_est185:*
155: gb_est186:*
156: gb_est187:*
157: gb_est188:*
158: gb_est189:*
159: gb_est190:*
160: gb_est191:*
161: gb_est192:*
162: gb_est193:*
163: gb_est194:*
164: gb_est195:*
165: gb_est196:*
166: gb_est197:*
167: gb_est198:*
168: gb_est199:*
169: gb_est200:*
170: gb_est201:*
171: gb_est202:*
172: gb_est203:*
173: gb_est204:*
174: gb_est205:*
175: gb_est206:*
176: gb_est207:*
177: gb_est208:*
178: gb_est209:*
179: gb_est210:*
180: gb_est211:*
181: gb_est212:*
182: gb_est213:*
183: gb_est214:*
184: gb_est215:*
185: gb_est216:*
186: gb_est217:*
187: gb_est218:*
188: gb_est219:*
189: gb_est220:*

190: gb_est221:*
191: gb_est222:*
192: gb_est223:*
193: gb_est224:*
194: gb_est225:*
195: gb_est226:*
196: gb_est227:*
197: gb_est228:*
198: gb_est229:*
199: gb_est230:*
200: gb_est231:*
201: gb_est232:*
202: gb_est233:*
203: gb_est234:*
204: gb_est235:*
205: gb_est236:*
206: gb_est237:*
207: gb_est238:*
208: gb_est239:*
209: gb_est240:*
210: gb_est241:*
211: gb_est242:*
212: gb_est243:*
213: gb_est244:*
214: gb_est245:*
215: gb_est246:*
216: gb_est247:*
217: gb_est248:*
218: gb_est249:*
219: gb_est250:*
220: gb_est251:*
221: gb_est252:*
222: gb_est253:*
223: gb_est254:*
224: gb_est255:*
225: gb_est256:*
226: gb_est257:*
227: gb_est258:*
228: gb_est259:*
229: gb_est260:*
230: gb_est261:*
231: gb_est262:*
232: gb_est263:*
233: gb_est264:*
234: gb_est265:*
235: gb_est266:*
236: gb_est267:*
237: gb_est268:*
238: gb_est269:*
239: gb_est270:*
240: gb_est271:*
241: gb_est272:*
242: gb_est273:*
243: gb_est274:*
244: gb_est275:*
245: gb_est276:*
246: gb_est277:*
247: gb_est278:*
248: gb_est279:*
249: gb_est280:*
250: gb_est281:*
251: gb_est282:*
252: gb_est283:*
253: gb_est284:*
254: gb_est285:*
255: gb_est286:*
256: gb_est287:*
257: gb_est288:*
258: gb_est289:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553.6	19.7	657	115	AM368381 PM2-HT019
2	541.2	19.2	582	115	AM368384 PM2-HT019
3	511	18.1	636	115	AM368377 PM2-HT019
4	485	17.2	637	115	AM368375 PM2-HT019
5	483	17.2	514	115	AM368378 PM2-HT019
6	467	16.6	517	115	AM382125 CM0-HT032
7	452.4	16.1	498	102	AI809318 we6a04.x
8	408.4	14.5	450	169	BE774398 284057 MA
9	406	14.4	541	139	BE752074 204371 MA
10	405.6	14.4	508	115	AM379296 MK0-HT024
11	393	13.9	569	118	AM605859 MK0-HT024
12	390.2	13.9	2045	192	AK017412 Mus muscu
13	385.6	13.7	565	115	AM379300 MK0-HT024
14	380.2	13.5	532	11	AA739350 vv51901.x
15	364.4	12.9	507	115	AM382186 CM0-HT032
16	359.6	12.8	595	146	BF303874 60188681
17	350.6	12.5	935	147	BF304617 601886019
18	343	12.2	613	164	BE201927 f103c02.x
19	341.6	12.1	697	165	BE295836 601176857
20	339	12.0	429	115	AM379322 MK0-HT024
21	313	11.1	656	164	BE201334 FK88D02.Y
22	302.6	10.7	967	146	BF304014 601886781
23	293.4	10.4	632	137	BE357417 f103c02.Y
24	292.8	10.4	609	120	AM767552 da78e02.Y
25	291.4	10.3	293	164	BE145042 PM4-HT019
26	276	9.8	895	106	AL528847 AL528847
27	272.4	9.7	421	139	BE706690 PM0-HT033
28	266.6	9.5	412	139	BE706715 PM0-HT033
29	262.4	9.3	371	115	AM382671 PM0-HT033
30	261.4	9.3	379	115	AM382639 PM0-HT033
31	261.4	9.3	394	115	AM382679 PM0-HT033
32	257.2	9.1	377	12	AA798748 vv07e06.x
33	255.6	9.1	400	115	AM382589 PM0-HT033
34	251	8.9	405	139	BE706691 PM0-HT033
35	247	8.8	875	144	BF101146 601754720
36	240.2	8.5	480	144	BF083249 RC1-CY024
37	238.8	8.5	403	117	AM503182 UT-HF-BNO
38	222.8	7.9	488	140	BE808133 213258 MA
39	219.2	7.8	341	115	AM382607 PM0-HT033
40	217.6	7.7	798	144	BE217496 fbn-1143
41	206.8	7.3	373	169	BF762307 f12-CS004
42	200.2	7.1	509	115	AM402694 UT-HF-BKO
43	199.6	7.1	738	112	AM174101 f139c06.Y
44	195.4	6.9	939	106	AL530477 AL530477
45	186.8	6.6	677	145	BF156068 f147b11.Y

## ALIGNMENTS

RESULT	1	EST	04-FEB-2000
AM368381	AM368381	657 bp	mRNA
LOCUS	PM2-HT0190-081099-001-d11	HT0190	Homo sapiens
DEFINITION	PM2-HT0190-081099-001-d11	HT0190	Homo sapiens
ACCESSION	AM368381		CDNA, mRNA sequence.
VERSION	AM368381.1	GI:6873031	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	HCGP <a href="http://www.ludwig.org.br/ORESTES">http://www.ludwig.org.br/ORESTES</a> .		
TITLE	The FAPESP/LICR Human Cancer Genome Project		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Simpson A.J.G.		
	Laboratory of Cancer Genetics		

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=PM2&t2=PM2-HT0190-081099-001-d11&t3=1999-10-08&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 573.  
Location/Qualifiers

## FEATURES

SOURCE  
1. 657  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="HT0190"  
/dev\_stage="Adult"  
/note="Organ: head,neck; Vector: puc18; Site:1: SmaI;  
Site:2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 192 a 157 c 163 g 145 t  
ORIGIN

Query Match 19.7%; Score 553.6; DB 115; Length 657;  
Best Local Similarity 98.8%; Pred. No. 1.6e-137;  
Matches 589; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

783 attcaagaggagacagattgccctctcagtcattgattcagtagaaggaggaagca 842  
1  
21 AATCAACGAGGAGGAGATG-CCTCTCTAGTCAATTGATTCAGTAGAGGAGCA 79  
843 tcccaagtgtgaaagatcccatcagaagaagagtgctgtaaccttaagacc 902  
1  
80 TCCCAGTGTGTAAGATCCATCAAGAGAGACAGATGCTGTGACTTATGAGCC 139  
903 a-ccccaagtgtgacatcagacagacagctctgtgacaattcattgtaacagca 961  
1  
140 ACCCCAGGTTGGCATGATTCACAGACAGCTGTGACATTTCACTTAACAGAGTT 199  
962 gtgttgaggagatgaacgcgcgtccaatttaacatgcttactctggaaccagagatg 1021  
1  
200 GTGTTGAGAGGATGAACCCGCTCCAAATTATCATTTGTTACTCTGGAACAGAGATG 259  
1022 ggcagatcctggcgcagacgtcttggagccgcagatcgtgcttggccaggaagaaga 1081  
1  
260 GGCAGTCTGTGGCCGACGCTGTTGAGCCGGGAGTCTGTGCTTGGCCAGAGAGACA 319  
1082 ggaagcgagatgaagatagatcagcaagaagcaagatttcgacagatcaagaacggtg 1141  
1  
320 GGAAGCGGATGAGATATATACAGAAACAGAGATTTCGGACAGTACAAAGACGCTG 379  
1142 atggttaagagcgcctgttgcacagacacatgtagtccagatgacatccatcaaga 1201  
1  
380 ATGTGTCGAAAGCGCCGCTTGTCTGCAACACATGTCAGATGATCATCATCAAGA 439  
1202 aacgaagatcccaagatgtaactgttattaccatgtaggggagcgtggaactatg 1261  
1  
440 AACGAGATCCCGAGTGTGATGATCTTTATCTTACATGAGGGCCCTGAGACTTATG 499  
1262 aatgctgttgaagatcaagaagtccttgaactcagtagtactcctcagcacaca 1321  
1  
500 AATGCTGTTGAAGATCAAGAGAGTCCCTGGAATCATGACAGTCTCTCAGACACAA 559  
1322 ttgaaagctacaggaacaa-gcaacagcagcagcagcagcacttacttcaagaaca 1376  
1  
560 TTGAAACGTACAGGCAACATGAAGACGACAGCACACGACCTTACTTCAAGAAACA 615

```

RESULT 2
LOCUS      AM368384      582 bp      mRNA      EST      04-FEB-2000
DEFINITION PM2-HT0190-081099-001-e08 HT0190 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM368384
VERSION     AM368384.1  GI:6873034
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 582)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE     The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM2&t2=PM2-HT0190-
            081099-001-e08&t3=1999-10-08&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 582.
FEATURES
    source
        1..582
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_1lb="HT0190"
            /dev_stage="Adult"
            /note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT      180 a      130 c      149 g      123 t
ORIGIN
Query Match      19.2%; Score 541.2; DB 115; Length 582;
Best Local Similarity 98.2%; Pred. No. 3,4e-134;
Matches 558; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Oy      811 agtcattgattcagatgagggaacacgcatcccgatgatagtgaagatcccatcaaa 870
        |||||||
Db       3 agtcattgattcagatgagggaacacgcatcccgatgatagtgaagatcccatcaaa 62

Oy      871 ggaagaacagagatgctgctggtacattatgagcca---ccccaggttgcaatgaatcaaga 928
        |||||||
Db       63 ggaagaacagagatgctgctggtacattatgagccaaccccaagtggtgcaatgaatcaaga 122

Oy      929 cagctcttgacaattcatcatggttaacaacagatgctgttgaggagatgaacccgcgtccaa 988
        |||||||
Db       123 cagctcttgacaattcatcatggttaacaacagatgctgttgaggagatgaacccgcgtccaa 182

Oy      989 tttaatactgttactctcgtgaacacagatggcgaagtcctctggccgcaagctctcttg 1048
        |||||||
Db       183 tttaatactgttactctcgtgaacacagatggcgaagtcctctggccgcaagctctcttg 242

Oy      1049 aggcccgagatctgctgcttgcccaagaagagacaggaagcgagatgaatatacaccagaa 1108
        |||||||
Db       243 aggcccgagatctgctgcttgcccaagaagagacaggaagcgagatgaatatacaccagaa 302

Oy      1109 agcaagaagtttcggaacgatacaagaacggtgatagtgtaagaagcgccgcttcgta 1168

```

```

Db       303 agcagcaagtttcgacagactacaaagacggtatgtagaagccgccgtttcgtaaca 362
        |||||||
Oy      1169 acacacatggtatccagatgacatccatcaagaagaagatccccaagatgatactgt 1228
        |||||||
Db       363 acacacatggtatccagatgacatccatcaagaagaagatccccaagatgatactgt 422

Oy      1229 ttacttaccagtgagggcgctgagactatgtaatctgcttgaaatcaagaagctcc 1288
        |||||||
Db       423 ttacttaccagtgagggcgctgagactatgtaatctgcttgaaatcaagaagctcc 482

Oy      1289 tggaaactcagtaagtaacctctcccaagacaaattgaacgtacagggcaacagcaagc 1348
        |||||||
Db       483 tggaaactcagtaagtaacctctctcccaagacaaattgaacgtacagggcaacagcaagc 542

Oy      1349 agcagcaccagcaacttacttcagaaca 1376
        |||||||
Db       543 agcagcaccagcaacttacttcagaaca 570

RESULT 3
LOCUS      AM368377/C      636 bp      mRNA      EST      04-FEB-2000
DEFINITION PM2-HT0190-081099-001-c08 HT0190 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM368377
VERSION     AM368377.1  GI:6873027
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 636)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE     The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM2&t2=PM2-HT0190-
            081099-001-c08&t3=1999-10-08&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 5
            High quality sequence stop: 635.
FEATURES
    source
        1..636
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_1lb="HT0190"
            /dev_stage="Adult"
            /note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT      139 a      150 c      155 g      192 t
ORIGIN
Query Match      18.1%; Score 511; DB 115; Length 636;
Best Local Similarity 99.0%; Pred. No. 4,5e-126;
Matches 514; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      858 agatccatcacaggaagacagagatgctggtacattatgagccacccaggttggcac 917
        |||||||

```

```

Db 629 AATCCATCAGAGAGACAGAGTGTGCTGCTTATGAGCCACCTCAGGTTGGCAG 570
Qy 918 TGAATCAGAGAGCTGTGATCAATTCATGTCAGAGCAATGTCAGAGGATGAG 977
Db 569 TGAATCAGAGAGCTGTGATCAATTCATGTCAGAGCAATGTCAGAGGATGAG 510
Qy 978 CCGCGTCCCAATTCATCAATTCATCAATTCATCAATTCATCAATTCATCAATTC 1037
Db 509 CCGCGTCCCAATTCATCAATTCATCAATTCATCAATTCATCAATTCATCAATTC 450
Qy 1038 AGCGTGTCTTGAAGCCCGGATCTGTGCTTGAAGCCCGGATCTGTGCTTGAAGCC 1097
Db 449 AGCGTGTCTTGAAGCCCGGATCTGTGCTTGAAGCCCGGATCTGTGCTTGAAG 390
Qy 1098 TAGCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1157
Db 389 TAGCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330
Qy 1158 GTTCGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1217
Db 329 GTTCGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 270
Qy 1218 TGATGAACTGTATCTTACCACTGAGTGGGGCCGTGAGACTTATGAATGCTGTGAA 1277
Db 269 TGATGAACTGTATCTTACCACTGAGTGGGGCCGTGAGACTTATGAATGCTGTGAA 210
Qy 1278 CAAAGAGTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1337
Db 209 CAAAGAGTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 150
Qy 1338 ACAAGAGTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1376
Db 149 ACAAGAGTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 111

RESULT 4
LOCUS AW368375 637 bp mRNA EST 04-FEB-2000
DEFINITION PM2-HT0190-081099-001-a07 HT0190 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW368375
VERSION AW368375.1 GI:6873025
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 637)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM2a2-PM2-HT0190-
081099-001-a07&cl=1999-10-08&cl=1)
Seq primer: puc18 forward
High quality sequence start: 14
High quality sequence stop: 589.
Location/Qualifiers
location=637
1. 637
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0190"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; site_1: SmaI;
site_2: SmaI; A mini-library was made by cloning products

```

```

BASE COUNT 136 a 146 c 161 g 194 t
ORIGIN
Query Match 17.2%; Score 485; DB 115; Length 637;
Best Local Similarity 98.8%; Pred. No. 4.3e-119;
Matches 499; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research).
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Qy 872 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 931
Db 628 GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
Qy 932 TCTGTACAAATTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 991
Db 569 TCTGTACAAATTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 510
Qy 992 TAATCATTTGTTACTCTGGAACAGAGATGTCAAGTCTTGAGGAGGAGGAGGAGG 1051
Db 509 TAATCATTTGTTACTCTGGAACAGAGATGTCAAGTCTTGAGGAGGAGGAGGAGG 450
Qy 1052 CCCGATCTGTCTGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1111
Db 449 CCCGATCTGTCTGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390
Qy 1112 AGCAAGTTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1171
Db 389 AGCAAGTTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330
Qy 1172 CACATGTTATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1231
Db 329 CACATGTTATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 270
Qy 1232 ACTTACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1291
Db 269 ACTTACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 210
Qy 1292 AACTCATGAGTACCTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1351
Db 209 AACTCATGAGTACCTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 150
Qy 1352 AGACCCAGCAGCTTACTTCAAGAAACA 125
Db 149 AGACCCAGCAGCTTACTTCAAGAAACA 125

RESULT 5
LOCUS AW368378 514 bp mRNA EST 04-FEB-2000
DEFINITION PM2-HT0190-081099-001-d01 HT0190 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW368378
VERSION AW368378.1 GI:6873028
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 514)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL:  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&tl2=PM2-HT0190-081099-001-d01&tl3=1999-10-08&tl4=1>)

Seq primer: puc 18 forward  
High quality sequence start: 20  
High quality sequence stop: 514.

## FEATURES

## SOURCE

1. 514

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="HT0190"

/dev\_stage="Adult"

/note="Organ: head\_neck; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## BASE COUNT

147 a 113 c 141 g 113 t

## ORIGIN

## Query Match

Best Local Similarity 98.8%; Pred. No. 1.4e-118; Score 483; DB 115; Length 514;

Matches 497; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 771 gctgagcgtgaattcaacgagggagacagatgcctcctagtcattgattcagtaga 830  
|||||  
DB 2 GCTGACCCCTGATTCACAGAGGACAGATGCCCCCTCCTAGCATTTGATTCAGATAGA 61

QY 831 ggggaacacgcatgcccagatgtatagaagatcccatcacagagaagacagatgtgtgt 890  
|||||  
DB 62 GGGGAACACGCAATGCCAGATGTAGAAGATCCCATCAAGAGACAGAGTGTGTGTGT 121

QY 891 acctatgagccaccccaaggttgcacgtcaattcaacagacgtctgtacatttcagt 950  
|||||  
DB 122 ACCTTATGAGCCACCCAGAGTGTGCATGATTCACAGACAGTTCATTCATTCATG 181

QY 951 taacagcaagttgtgttggagggatgaacgcgcgtcccaatttaatttgaatttcgtga 1010  
|||||  
DB 182 TAAACACAGATGTTGGAGGAGATGTAAGATCCCATCAAGAGACAGAGTGTGTGTGT 241

QY 1011 aaccagaagatggcgaagtccttggcgaacgtgcttggagcccgagatctgtgtgtgccc 1070  
|||||  
DB 242 AACCAAGATGGGCAAGTCTTG6GCCGACGCTGCTTTGAG6GCCGAGTCTGTGCTTGC 301

QY 1071 aggaagaagacaggaagcgagatgaatagatcagaaagcaagtttcgagacagtac 1130  
|||||  
DB 302 AGGAAGAAGACAGGAAGCGGATGATGATGATGATGATGATGATGATGATGATGATG 361

QY 1131 aaagaacggtgtggtgaagaagcgccgttctgtcagaacacatggtatccagatgtac 1190  
|||||  
DB 362 AAAGAACGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421

QY 1191 atccatcaagaagaagatcccatgagatgagacgttatacttaactcaggttagggcg 1250  
|||||  
DB 422 ATCCATCAAGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 480

QY 1251 tgaagactatgaagatgctgttga 1273  
|||||  
DB 481 TGAGACTTATGCAATGCTGCTGA 503

RESULT 6

LOCUS AW382125 517 bp mRNA EST 04-FEB-2000  
DEFINITION CM0-HT0322-201299-135-e02 HT0322 Homo sapiens CDNA, mRNA sequence.

ACCESSION AW382125  
VERSION AW382125.1 GI:6886784

KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 517)

## AUTHORS

HCGP <http://www.ludwig.org.br/ORESTES>.

## TITLE

The FAPESP/LICR Human Cancer Genome Project

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&tl2=CM0-HT0322-201299-135-e02&tl3=1999-12-20&tl4=1>)

Seq primer: puc 18 forward

High quality sequence start: 38

High quality sequence stop: 517.

## FEATURES

## SOURCE

1. 517

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="HT0322"

/dev\_stage="Adult"

/note="Organ: head\_neck; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## BASE COUNT

146 a 123 c 140 g 108 t

## ORIGIN

## Query Match

Best Local Similarity 95.7%; Pred. No. 2.8e-114; Score 467; DB 115; Length 517;

Matches 506; Conservative 0; Mismatches 10; Indels 13; Gaps 2;

QY 680 caccctccagagagctgtatccgcgcacatcctgctacaaaagctagacgtca 739  
|||||  
DB 1 CAACCTCCTCGGAGCTGTATCCGCGCATCTGCTCTACAAAAGCTGACGCTCA 60

QY 740 cgaagtggtgaagcgtgtcccaaccatgagctgagccgtgaattcaacgagagaca 799  
|||||  
DB 61 CGAGGTGTGTAAGCGGTGCCCAACCATGACCTGAGCCGTGAATTCAGAGGACAGA 120

QY 800 ttgcccctcctgattgattgagtagagaggaagacacatgccccagratgagaag 859  
|||||  
DB 121 TTGCCCTCTCTGATATTTGATTCAGTAGAGGGAACAGCCATCCCAATGATGTAAG 180

QY 860 atcccatcagaagaagacagatgtgtcgtgtacctaataagaccacccaggttgcagct 919  
|||||  
DB 181 ATCCCATCAGAGAAGACAGATGTGTGATCTTATGAGCACCCAGGTGTGCACTG 240

QY 920 aattcagacagctctgtac-aattcatgttcaacagcagttgtgttggagatgaac 978  
|||||  
DB 241 AATTACGACAGCTTGTGTAACAATTTCAATGATGATGATGATGATGATGATGATG 300

QY 978 cgcgtcgaattatatactgttactcctggaacacagatggcgaagtcctgtggccga 1038  
|||||  
DB 301 CGCCGCTCAATTTTATCTTGTACTGTGGAACAGAGATGGCAAGTCTTG6GCCGA 360

QY 1038 cgcgtccttgaagcccgagatcgtgtcttgcaggaagaagacaggaagcgagatagaat 1098  
|||||  
DB 361 CGCTGCTTTGAGGCCGAGATCTGTGCTTCCAGGAAGAAGACAGGAGCGATGAAGAT 420

QY 1098 agcatcagaagaagcaggaatttcgagacagttacaaagcagtgatgttgaagacgccc 1158  
|||||



Db 421 AGCATCAGAAACAGCAAGTTTCGACACTACAAAGACGGTGATG-----CG 468

Qy 1159 ttctgtcagaacacacatggtatccagatgacatccatcaagaacgaa 1207  
|||||  
Db 469 TTTGCGTACAGACACTATGATTCACGATGACATCCATCAGAAACGAA 517

RESULT 7  
LOCUS A1809318 498 bp mRNA EST 18-DEC-1999  
DEFINITION we6a04.x1 Soares\_NFL.T.GBC.S1 Homo sapiens cDNA clone  
IMAGE:2348910 3', mRNA sequence.  
ACCESSION A1809318  
VERSION A1809318.1 GI:5395884  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 498)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1013 Std Error: 0.00  
Seq primer: -40UP from Glibco  
High quality sequence stop: 446.  
FEATURES  
source  
1. 498  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="2348910"  
/clone\_lib="Soares\_NFL.T.GBC.S1"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with  
a modified polylinker; Site.1: Not I; Site.2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCL-CGAP-GCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 172 a 73 c 100 g 153 t  
ORIGIN

Query Match 16.1%; Score 452.4; DB 102; Length 498;  
Best Local Similarity 97.0%; Pred. No. 2.3e-110;  
Matches 483; Conservative 0; Mismatches 11; Indels 4; Gaps 2;

Qy 2318 cagtaataatgccctagtagttgtaccatattcaagctcaaatgaa 2377  
|||||  
Db 498 CAGTATATATGCCCTTACTAGTTGTTTACCATTTTCAAACTCAAAATAGATTTGAA 439

Qy 2378 gccctctcaacaactctgataatttcttaattagagctcttccctcaagctac 2437  
|||||  
Db 438 GCCCTCTCCAAAATCTGTGATTAATTTCTTAATAGACTTCTATCCCTCAAGCTTAC 379

Qy 2438 ctaccataaacaacagccatattactgatactgttcagttcattagccagagacttacc 2497  
|||||  
Db 378 CTACCATTAATAACAGCATATATAGTACTGTGAGTTCATTTAGCCAGAGACTTACG 319

Qy 2498 ttcttgatagtagagatccaaagcagagcgtgtcaaaatcagcactctgtcgtgaataa 2557  
|||||  
Db 318 TTTTGAGTAAAGTAGATCCAAAGCAGCTGTAAATCAAGCACTCCTGAGCTGGAATTA 259

Qy 2558 aagatgaaaggtagactacttttcttttltta--ctcaaaaglttagaagatctcg 2615  
|||||  
Db 258 AAGATGAAAGGGTAGACTACTTTCTTTTAACTCAAAAAGTTTAGAGATCTCG 199

Qy 2616 ttctcttccattttaaacaatatttaagaataatagataaagactttaaagttcc 2675  
|||||  
Db 198 TTTCTTTTCATTTTAAACATATATTTTAAATAGATTAAGATTAAGACTTTTAAATGTTTC 139

Qy 2676 tccctccatcttccacaccagctacagcagctatttctgtcaccagacaatga 2735  
|||||  
Db 138 TCCCTCCATCTTCCACACCCAGTACACGACGATATTTCTGTGACCAAGACATATA 79

Qy 2736 ttctgttatgagcgtgtgtcttctgtgat--gtgtgatttcaatttcaataact 2793  
|||||  
Db 78 TTTCTTGTATTAGAGCTGTGCTTGTAGTAATCCGCCGATATTTTCAATTAAC 19

Qy 2794 ttgtcatcttggtttaa 2811  
|||||  
Db 18 TTTGCAATTTGTTTAA 1

RESULT 8  
LOCUS BF774398 450 bp mRNA EST 12-JAN-2001  
DEFINITION 284057 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BF774398  
VERSION BF774398.1 GI:12122298  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 450)  
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,  
Bennett,G.A., Fahrnerkrug,S.C., Fieking,B.A., Rohrer,G.A., Laegreid  
W.M. and Keele,J.W.  
Design and use of four pooled tissue normalized cDNA libraries for  
EST discovery in cattle  
Unpublished (2000)  
CONTACT: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithemail.marc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross-match with the -mnscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCGAGTCACGACG  
Plate: 83 row: C column: 20  
Seq primer: ATTGTAGTGACACTATAG.  
FEATURES  
source  
1. 450  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC 3BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORF6; Site.1: XbaI; Site.2: XhoI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."  
BASE COUNT 130 a 122 c 113 g 85 t  
ORIGIN

Query Match 14.5%; Score 408.4; DB 169; Length 450;  
Best Local Similarity 94.2%; Pred. No. 1.5e-98;  
Matches 424; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Oy	1020	tgaggaaatccctgggcccagacctgctttgagcccggaatctgtgcttcccaagaaga	1079
Db	1	tgggcaatgctctggggcccccctgcttggtagcccggaatctgtgcttcccaagaaga	60
Oy	1080	caggaaggccggaatgaagataagatcaagaagaagcgaatttcgagcagtacaaagacgg	1139
Db	61	caggaaagccggaatgaagataagatcaagaagaagcgaatttcgagcagtacaaagacgg	120
Oy	1140	tgatgtatcggaagggcccggtttcgfcaaaagaacataigtatcgaatgacatccatga	1199
Db	121	tgatgtatcggaagggcccggtttcgfcaaaagaacataigtatcgaatgacatccatga	180
Oy	1200	gaagaagaatccccagatatgatactgttatacttaccagtgaagggccgttgaaactta	1259
Db	181	gaagaagaatccccagatatgatactgttatacttaccagtgaagggcccgtagaactta	240
Oy	1260	tgaatgtctgttgaagaatcaaaagagtcctcggaactatgcagtcactctctcagcaac	1319
Db	241	cgaaatgtcgtcgaagaatcmaaaagatccctggaaactatgcagtcactctcagcaac	300
Oy	1320	aattgaacgtatcaggaacaacagcaacagcagcagcaacgaacttaactcagaacatct	1379
Db	301	gatttgaacacttaccagcaccacagcaacagcagcaacgaacttaacttcaaaacatct	360
Oy	1380	cccttcagccctgcttcaagaatgaagctgtgtgagcccgagagaagaactccaacaatc	1439
Db	361	cccttcagcccttctcaggaatgaagctgtgtgagcccgagagaagaactccaacaatc	420
Oy	1440	tgaacttctcttagaacttccaagccccc	1469
Db	421	tgaacgcttcttagaacttccaagccccc	450

**FEATURES**  
**source**

```

5 row: M column: 16
er: ATTATGGGACACATATG.
Location/Qualifiers
1. 541
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2B0Y"
/tissue_type="pooled"

```

```

/ab_host="DH10B"
/notes="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI
Library made from pooled tissue from testis, thymus,
semimandibular muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT      149 a      132 c      133 g      127 t
ORIGIN

```

Query Match	14.4%	Score 406;	DB 139;	Length 541;
Best Local Similarity	90.6%	Pred. No. 6.9e+98;		
Matches 433;	Conservative	0;	Mismatches 45;	Indels 0;
			Gaps	0

Oy	1086	ggcggaatgaagatagatcatcgaagaagcgaagtcttcggacatcaagaacggttgatgg	1145
Db	1	GGCGGATGAAGATATGCATCTCGAAGACGACGAGGTCTTCGGACACACAAAGATGGTGATGG	60
Oy	1146	tacgaagcgcccgcttcgttcagacacacatggtatccagatgataccatcaagaagc	1205
Db	61	TACGAAGCGCCCTTCGTCGACGACACACATGGCATCCGAGATGCATCATCAAGAAACG	120
Oy	1206	aagatcccccagatgataactgctttacttaccagtgaagggcgttgagacttataaat	1265
Db	121	AAGATCCCCAGATGATGAACTGTTATTACTTACCAAGTAAAGGGCCGTGAGACTTACGAAT	180
Oy	1266	gctctgtaagatcaagaagagtcctcttggaactcatgcaagtaacctcttcacgaacaatgta	1325
Db	181	GCTGOTGAAGATCAAAAGATTCCTCGGAACATCAAGCATCTCTCCAGACACAGATTGA	240
Oy	1326	aacgtacagcgaacagaacaaacagcaagaacacccagcacttacttgaaanaactctcccttc	1385
Db	241	AACCTACGCGAGGAGGAGGACGACACGACACTTACTTTCAGAAACATCTCTTTC	300
Oy	1386	agccgcttcacgaatagactctgtgagccccggagagagaactccaaacaactctgacgt	1445
Db	301	AGCCGCTTCAAGAAATAGCTTGTGGAGCCGGGAGAGAAACCCGAGACATCTGACGC	360
Oy	1446	ctctcttagacatcccaagcccccaacacgaatcagtgatcccatagagacctatctcat	1505
Db	361	CTTCTTTAGACATTCGAGTCCGCCCAATCATCATAGTACCATAGAGCCCATCTGCT	420
Oy	1506	attttaagtggtgtgtgatatccatccatgtagtatatgtagtgctgtgtgtatgt	1563
Db	421	ATTTTGAGATGATGCTTTATGTGTCTTCTGTGTGTGTGTGACAGTGTGTGAGATGT	478

RESULT	10
AM379296	
LOCUS	AM379296 508 bp mRNA EST 04-FEB-2000
DEFINITION	MRO-HR0241-091299-004-b02 HR0241 Homo sapiens cDNA, mRNA sequence
ACCESSION	AM379296
VERSION	AM379296.1 GI:6883955
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 508) HCGP <a href="http://www.ludwig.org.br/ORESTERIS">http://www.ludwig.org.br/ORESTERIS</a> . The FAPESP/LICR Human Cancer Genome Project Unpublished (1999) Contact: Simpson A.J.G.
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel.: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL:  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&lt2=MR0-HT02411>)  
(091299-004-b02&lt3=1999-12-09&lt4=1)





Db 544 GACCATATACGGGACCAAGGCTCTGAATGAAGTAACACCAAAAATGAGACTCCAGC 603  
 Oy 1150 aagagcccgcttcgtcagaacacacatggtat-----ccagatgacatccatcaagaa 1203  
 Db 604 AAGCGTGCATTCACAGACAGAGCCCTCCATCCCTCCCTGGGTACCACTGAAGAG 663  
 Oy 1204 cgaagatcccccagatgaaactgttacttaccagtgagggcgagagactatgaa 1263  
 Db 664 AGACCCACGGGGAGAGAGATGTTCTACATGACAGTGCGGGGAGAGAACTTTGAG 723  
 Oy 1264 atgctgttgaagatcaagaagtcctcgtgaactatgacatccttcctcagacacaatt 1323  
 Db 724 ATCTTGATGAAGATCAAGAGAGAGCTAGATGATGAGCTTGCCCAAGCTTTGGTT 783  
 Oy 1324 gaacgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1383  
 Db 784 GACCTCTATCAGACAGACAGCAGCAGCAGCTCTCTACAGAGCCGAGTACCTGCAGCCT 843  
 Oy 1384 tcagcct 1390  
 Db 844 CCATCCT 850

## RESULT 13

AM379300 565 bp mRNA EST 04-FEB-2000  
 LOCUS MRO-HT0241-101299-003-a05 HT0241 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AM379300  
 VERSION AM379300.1 GI:6883959  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
 TITLE HCGP <http://www.ludwig.org.br/ORESTES>.  
 JOURNAL The FAPESP/LICR Human Cancer Genome Project  
 COMMENT Unpublished (1999)  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1-MR0&l2-MR0-HT0241-101299-003-a05&l3-1999-12-10&l4-1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 52  
 High quality sequence stop: 331.  
 Location/Qualifiers

## FEATURES

source  
 1. 565  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="HT0241"  
 /dev\_stage="Adult"  
 /note="Organ: head\_neck; Vector: puc18; Site: 1: Sma1;  
 Site: 2: Sma1; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 Profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT 178 a 126 c 140 g 121 t  
 ORIGIN

Query Match 13.7%; Score 385.6; DB 115; Length 565;  
 Best Local Similarity 95.7%; Pred. NO. 2.1e-92;  
 Matches 440; Conservative 0; Mismatches 14; Indels 6; Gaps 4;

Oy 923 tcagcagctctgtacacatttcacatgtgtaaac -gcagttgtgttgagggatgaaccgc 981  
 Db 7 TCACGACAGTCTTTGATGATTCATGTTAAACACCAGTGTGTTGGAGGATGAACCGC 66  
 Oy 982 cgtccatttaacatctgtactctgtgaaacagagatgtgcaagtcctgtgcccagc 1041  
 Db 67 CGTCAATTTTAAATATCTTCTCTGGAACCAAGATGGCAAGTCTGTGGCCGAGC 126  
 Oy 1042 tgccttggagcccgagatcgtgtgtgtccaggaagagacaggaagcgatgaatagc 1101  
 Db 127 TGCTTTGAGGCCCGGATGCTGTCTTGCCAGAGAGACAGAGAGCGGATGAATAGC 186  
 Oy 1102 atcgaagaagcgaagatcttcgacagatcaagaacagtgatgtgaagagcgccgttt 1161  
 Db 187 ATCAGAAAGCAGCAAGTTTGGACAGTAAAGAGGATGATGATGAGAGCGCCGTTT 246  
 Oy 1162 cgtcagaacacacatgcatcag -atgacatccatcaagaacgaagatccagatg 1219  
 Db 247 CGTCAAGACACACATGTTATCCAGATGACCATCCATCAGAAACGAGATCCCAAGATG 306  
 Oy 1220 atgaactgttacttaccagtgagggcggtgagact -atgaactgtgtgaagat 1277  
 Db 307 ATGAAGTGTATATCTTACACAGTGAAGGGCGCGAGACATTATGAACATGCTTTGAAGAT 366  
 Oy 1278 caaagaagtcctcgtgaactcagtcagctactcctca -gcacacattgaagctacagc 1336  
 Db 367 CAAAGAGTCCCGGAGACATCATCTTCACTTCTCAGGAAACAATTTGAAGGTACAGGC 426  
 Oy 1337 aacgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1376  
 Db 427 AACACACACAGCAGAGAGACACACACTTACTTCAAGAACCA 466

## RESULT 14

AA739350 532 bp mRNA EST 14-JAN-1998  
 LOCUS v51g01.r1 Soares\_thymus\_2nbmt Mus musculus cDNA clone  
 DEFINITION IMAGE:1225968 5', mRNA sequence.  
 ACCESSION AA739350  
 VERSION AA739350.1 GI:2775536  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Mammalia; Euthera; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.  
 TITLE The Washu-HHMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 Washu-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: [mousetest@wustl.edu](mailto:mousetest@wustl.edu)  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 MGI:651560  
 Seq primer: -28m3 rev2 ET from Amersham  
 High quality sequence stop: 508.  
 Location/Qualifiers

## FEATURES

source  
 1. 532  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_image="IMAGE:1225968"  
 /clone\_lib="Soares\_thymus\_2nbmt"



Wed Aug 8 08:03:56 2001

us-09-670-568b-2.rst

Page 13

Search completed: August 7, 2001, 22:52:06  
Job time: 8102 sec

---

**This Page Blank (uspto)**